U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

# SEARCH REQUEST FORM

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Date: _____ Phone: _____ Art Unit: _____

**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 02-24-03

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CPU time: _____

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**Search Site**

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_____ Pre-S

**Type of Search**

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

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_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGN

Jiang, D.
09/608918
Seq. ID 2

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 24, 2003, 09:19:21 ; Search time 39 Seconds
(without alignments)
2364.344 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLSLALGRSPVVLS.....TPAPGRGVGPGAGPGAGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3716 | 100.0 | 692 | 22 | AAB61880 | Human cytokine rec |
| 2 | 3716 | 100.0 | 692 | 23 | AAE14562 | Human cytokine rec |
| 3 | 3699.5 | 99.6 | 705 | 22 | AAU29322 | Human PRO polypept |
| 4 | 3699.5 | 99.6 | 705 | 22 | AAU04956 | Human Interleukin |
| 5 | 3699.5 | 99.6 | 705 | 22 | AAB87606 | Human PRO20040. H |
| 6 | 3699.5 | 99.6 | 705 | 22 | AAB61884 | Chimeric Zcytor14 |
| 7 | 3699.5 | 99.6 | 705 | 23 | ABB95604 | Human angiogenesis |
| 8 | 3699.5 | 99.6 | 705 | 23 | ABB84998 | Human PRO20040 pro |
| 9 | 3695.5 | 99.4 | 705 | 23 | AAU98792 | Human interleukin |
| 10 | 3654 | 98.3 | 720 | 23 | AAU98781 | Human full length |
| 11 | 3604.5 | 97.0 | 675 | 22 | AAB61885 | Chimeric Zcytor14 |
| 12 | 3588 | 96.6 | 688 | 22 | AAB61883 | Chimeric Zcytor14 |
| 13 | 3566.5 | 96.0 | 703 | 23 | AAU98791 | Human interleukin |
| 14 | 3535.5 | 95.1 | 703 | 23 | AAU11353 | Human DNAX cytokin |
| 15 | 3510.5 | 94.5 | 693 | 23 | AAU98790 | Human interleukin |
| 16 | 3445.5 | 92.7 | 683 | 23 | AAU98789 | Human interleukin |
| 17 | 2971 | 80.0 | 575 | 22 | AAB61881 | Human variant Zcyt |
| 18 | 2576.5 | 69.3 | 553 | 23 | AAU98788 | Human interleukin |
| 19 | 2410.5 | 64.9 | 698 | 23 | AAU11354 | Mouse DNAX cytokin |
| 20 | 2408.5 | 64.8 | 698 | 23 | ABB72297 | Murine protein iso |
| 21 | 2400.5 | 64.6 | 698 | 23 | AAU99161 | Mouse interleukin |
| 22 | 2389.5 | 64.3 | 698 | 23 | AAE14560 | Murine cytokine re |
| 23 | 2352.5 | 63.3 | 674 | 23 | AAE14559 | Murine cytokine re |
| 24 | 2006.5 | 54.0 | 409 | 23 | AAU98787 | Human interleukin |
| 25 | 1886 | 50.8 | 372 | 23 | AAU98786 | Human interleukin |
| 26 | 1714.5 | 46.1 | 348 | 23 | AAU98785 | Human interleukin |
| 27 | 1432 | 38.5 | 309 | 21 | AAY76143 | Human secreted pro |
| 28 | 1365.5 | 36.7 | 332 | 23 | AAU98784 | Human interleukin |
| 29 | 1305 | 35.1 | 267 | 22 | AAB88448 | Human membrane or |
| 30 | 1300 | 35.0 | 332 | 22 | AAM25864 | Human protein sequ |
| 31 | 1266 | 34.1 | 269 | 23 | AAU98783 | Human interleukin |
| 32 | 1079 | 29.0 | 204 | 22 | AAE10920 | Human gene 12 enco |
| 33 | 933 | 25.1 | 186 | 23 | AAU98782 | Human interleukin |
| 34 | 326.5 | 8.8 | 617 | 21 | AAY76048 | Murine skin cell p |
| 35 | 326.5 | 8.8 | 617 | 22 | AAB55987 | Skin cell protein, |
| 36 | 326.5 | 8.8 | 617 | 23 | ABB72187 | Murine protein iso |
| 37 | 309.5 | 8.3 | 667 | 22 | AAU04957 | Human Interleukin |
| 38 | 309.5 | 8.3 | 667 | 23 | AAU83601 | Human PRO protein, |
| 39 | 304.5 | 8.2 | 657 | 23 | AAU11356 | Human DNAX cytokin |
| 40 | 174 | 4.7 | 866 | 17 | AAW04185 | Human interleukin- |
| 41 | 174 | 4.7 | 866 | 19 | AAW61272 | Human interleukin- |
| 42 | 174 | 4.7 | 866 | 20 | AAW92409 | Human IL-17R prote |
| 43 | 174 | 4.7 | 866 | 21 | AAY99941 | Human IL-17R prote |
| 44 | 174 | 4.7 | 866 | 21 | AAY97131 | Human interleukin- |
| 45 | 174 | 4.7 | 866 | 21 | AAY97181 | Human interleukin- |

ALIGNMENTS

RESULT 1
AAB61880
ID AAB61880 standard; Protein; 692 AA.
XX
AC AAB61880;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human cytokine receptor Zcytor14.
XX
KW Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW antiinflammatory; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200104304-A1.
XX
PD 18-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18383.
XX
PR 07-JUL-1999; 99US-0348854.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Burkhead SK, Pownder SL;
XX
DR WPI; 2001-112618/12.
DR N-PSDB; AAC85027.
XX
PT New polypeptide encoding a human cytokine receptor Zcytor14, for
PT treating inflammation e.g. rheumatoid arthritis -
XX

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PS   Claim 2; Page 2; 112pp; English.
XX
CC   The invention provides a new human cytokine receptor desinated Zcytor14.
CC   Zcytor14 can be expressed by standard recombinant methodology. The
CC   encoding nucleic acid is useful for detecting the expression of a
CC   Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC   used to screen biological samples in vitro for the presence of Zcytor14.
CC   Proteins, polypeptides and peptides having Zcytor14 activity can be
CC   administered to a subject who lacks an adequate amount of this
CC   polypeptide, for treating inflammation and conditions such as rheumatoid
CC   arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC   antibodies) can be used to treat a subject who produces an excess of
CC   Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC   Zcytor14 to a subject. The present sequence represents the human
CC   cytokine receptor Zcytor14.
XX
SQ   Sequence   692 AA;

  Query Match            100.0%;  Score 3716;  DB 22;  Length 692;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
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Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480

Qy     481 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 540
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Db     481 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 540

Qy     541 QTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGS 600
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Db     541 QTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGS 600

Qy     601 YVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAL 660
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Db     661 QPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692


RESULT 2
AAE14562
ID   AAE14562 standard; Protein; 692 AA.
XX
AC   AAE14562;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human cytokine receptor Zcytor14.
XX
KW   Murine; cytokine receptor; Zcytor14; inflammation; rheumatoid arthritis;
KW   gene therapy; protein therapy; human; receptor.
XX
OS   Homo sapiens.
XX
PN   WO200204519-A2.
XX
PD   17-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US21344.
XX
PR   06-JUL-2000; 2000US-216446P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Gao Z;
XX
DR   WPI; 2002-179701/23.
XX
PT   New murine cytokine receptor, Zcytor14, and polynucleotides encoding
PT   the receptor, useful for treating inflammation, specifically rheumatoid
PT   arthritis, and as educational tools or in research -
XX
PS   Disclosure; Page 98-99; 99pp; English.
XX
CC   The invention relates to murine cytokine receptor, Zcytor14.
CC   The Zcytor14 polypeptide is useful for identifying or isolating
CC   Zcytor14 ligands, in preparing antibodies, in identifying proteins or
CC   peptide cleavage sites, in amino acid sequence analysis, and in
CC   monitoring biological activities of both the native and tagged protein in
CC   vitro or in vivo. Polypeptides having Zcytor14 activity can be used to
CC   treat inflammation, such as rheumatoid arthritis. Zcytor14 polynucleotide
CC   may be used as educational tool in genetics, molecular biology,
CC   protein chemistry and antibody production analysis, in the preparation
CC   of expression constructs for bacterial, viral or mammalian expression,
CC   in determining mRNA and DNA localisation of Zcytor14 polynucleotide in
CC   tissues, for identifying related polynucleotides and polypeptides by
CC   nucleic acid hybridisation, in linkage-based testing for various
CC   diseases in murine models, and to determine whether a subject's
CC   chromosomes contain a mutation in the Zcytor14 gene. Zcytor14
CC   oligonucleotide probes are useful for in vivo diagnosis, and for
CC   detecting and localising Zcytor14 gene expression in tissue samples.
CC   The present sequence is human cytokine receptor, Zcytor14 which can
CC   be used to generate humanised variant of murine Zcytor14 sequence.
XX
SQ   Sequence   692 AA;

  Query Match            100.0%;  Score 3716;  DB 23;  Length 692;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
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Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
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Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
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Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
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Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480

Qy     481 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 540
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Db     481 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 540

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     601 YVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAL 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 YVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAL 660

Qy     661 QPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           ||||||||||||||||||||||||||||||||
Db     661 QPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692


RESULT 3
AAU29322
ID   AAU29322 standard; Protein; 705 AA.
XX
AC   AAU29322;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PRO polypeptide sequence #299.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06520.
XX
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-187202P.
PR   06-MAR-2000; 2000US-186968P.
PR   14-MAR-2000; 2000US-189320P.
PR   14-MAR-2000; 2000US-189328P.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000US-190828P.
PR   21-MAR-2000; 2000US-191007P.
PR   21-MAR-2000; 2000US-191048P.
PR   21-MAR-2000; 2000US-191314P.
PR   28-MAR-2000; 2000US-192655P.
PR   29-MAR-2000; 2000US-193032P.
PR   29-MAR-2000; 2000US-193053P.
PR   30-MAR-2000; 2000WO-US08439.
PR   04-APR-2000; 2000US-194449P.
PR   04-APR-2000; 2000US-194647P.
PR   11-APR-2000; 2000US-195975P.
PR   11-APR-2000; 2000US-196000P.
PR   11-APR-2000; 2000US-196187P.
PR   11-APR-2000; 2000US-196690P.
PR   11-APR-2000; 2000US-196820P.
PR   18-APR-2000; 2000US-198121P.
PR   18-APR-2000; 2000US-198585P.
PR   25-APR-2000; 2000US-199397P.
PR   25-APR-2000; 2000US-199550P.
PR   25-APR-2000; 2000US-199654P.
PR   03-MAY-2000; 2000US-201516P.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   05-JUN-2000; 2000US-209832P.
PR   28-JUL-2000; 2000WO-US20710.
PR   22-AUG-2000; 2000US-0644848.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS46223.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumours, such as prostate and breast tumours, in mammals and
PT   to screen for modulators of the compounds -
XX
PS   Claim 11; Fig 598; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders.
XX
SQ   Sequence   705 AA;

  Query Match             99.6%;  Score 3699.5;  DB 22;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
```

```
Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
```

```
RESULT 4
AAU04956
ID   AAU04956 standard; Protein; 705 AA.
XX
AC   AAU04956;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human Interleukin 17 receptor, IL-17RH2.
XX
KW   Human; Interleukin-17 receptor; IL-17RH2; agonist; antagonist;
KW   PRO20040; DNA 164625-2890; systemic lupus erythematosus;
KW   rheumatoid arthritis; osteoarthritis; diabetes mellitus;
KW   allergic disease; asthma; demyelinating disease;
KW   degenerative cartilaginous disorder; transplantation associated disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Signal_peptide
FT   Protein         21..705
FT                   /label= Mature_IL_17RH2
FT   Region          107..112
FT                   /note= "N-myristoylation site"
FT   Modified-site   118..121
FT                   /note= "Asn is N-glycosylated"
FT   Region          152..157
FT                   /note= "N-myristoylation site"
FT   Modified-site   186..189
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   198..201
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   211..214
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   238..241
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   248..251
FT                   /note= "Asn is N-glycosylated"
FT   Region          319..324
FT                   /note= "N-myristoylation site"
FT   Modified-site   334..337
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   357..360
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   391..394
FT                   /note= "Asn is N-glycosylated"
FT   Region          438..443
FT                   /note= "N-myristoylation site"
FT   Domain          453..473
FT                   /note= "Transmembrane domain"
FT   Region          516..521
FT                   /note= "N-myristoylation site"
FT   Region          552..555
FT                   /note= "cAMP/GMP-dependent protein kinase
FT                   phosphorylation site"
FT   Region          583..586
FT                   /note= "Glycosaminoglycan attachment site""
FT   Region          612..617
FT                   /note= "N-myristoylation site"
FT   Region          692..697
FT                   /note= "N-myristoylation site"
FT   Region          696..701
FT                   /note= "N-myristoylation site"
FT   Region          700..705
FT                   /note= "N-myristoylation site"
XX
PN   WO200146420-A2.
XX
PD   28-JUN-2001.
XX
PF   20-DEC-2000; 2000WO-US34956.
XX
PR   23-DEC-1999;   99US-0172096.
PR   30-DEC-1999;   99WO-US31274.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   02-MAR-2000; 2000WO-US05841.
PR   21-MAR-2000; 2000US-0191007.
PR   21-MAR-2000; 2000WO-US07532.
PR   02-JUN-2000; 2000WO-US15264.
PR   22-JUN-2000; 2000US-0213087.
PR   22-AUG-2000; 2000US-0644848.
PR   24-AUG-2000; 2000WO-US23328.
PR   24-OCT-2000; 2000US-0242837.
PR   10-NOV-2000; 2000WO-US30873.
PR   28-NOV-2000; 2000US-0253646.
PR   01-DEC-2000; 2000WO-US32678.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Chen J,  Filvaroff E,  Fong S,  Goddard A,  Godowski PJ,  Grimaldi CJ;
PI   Gurney AL,  Li H,  Hillan KJ,  Tumas D,  Van Lookeren M,  Vandlen RL;
PI   Watanabe CK,  Williams PM,  Wood WI,  Yansura DG;
XX
DR   WPI; 2001-451708/48.
DR   N-PSDB; AAS09515.
XX
PT   Novel PRO polypeptides homologous to interleukin-17, useful for the
PT   diagnosis and treatment of immune related disease e.g. rheumatoid
PT   arthritis and diabetes -
XX
PS   Claim 10; Fig 14; 188pp; English.
XX
CC   The sequence is PRO20040 which is the human Interleukin 17 receptor,
CC   IL-17RH2, encoded by DNA 164625-2890. A composition
CC   containing ant/agonists to the PRO polypeptides or individual components
CC   are useful for treating a mammal with an immune related disease, e.g.
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CC   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC   juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC   idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC   vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC   thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC   disease, a demyelinating disease, an autoimmune or immune-mediated skin
CC   disease, contact dermatitis, an allergic disease e.g. food
CC   hypersensitivity, asthma, a transplantation associated disease, or a
CC   chronic inflammatory demyelinating polyneuropathy. Treating a
CC   degenerative cartilaginous disorder comprises administering a PRO1031 or
CC   PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
CC   examples of the diseases and disorders are given in the specification.
XX
SQ   Sequence   705 AA;

  Query Match             99.6%;  Score 3699.5;  DB 22;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 5
AAB87606
ID   AAB87606 standard; Protein; 705 AA.
XX
AC   AAB87606;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO20040.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   07-DEC-1999;   99US-0169495.
PR   09-DEC-1999;   99US-0170262.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   03-MAR-2000; 2000US-0187202.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   05-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92138.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping. -
XX
PS   Claim 12; Fig 162; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping.
XX
SQ   Sequence   705 AA;

  Query Match             99.6%;  Score 3699.5;  DB 22;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
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Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy    528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
```

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RESULT 6
AAB61884
ID   AAB61884 standard; Protein; 705 AA.
XX
AC   AAB61884;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Chimeric Zcytor14 protein #2.
XX
KW   Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW   antiinflammatory; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO200104304-A1.
XX
PD   18-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US18383.
XX
PR   07-JUL-1999;   99US-0348854.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Burkhead SK,  Powder SL;
XX
DR   WPI; 2001-112618/12.
XX
PT   New polypeptide encoding a human cytokine receptor Zcytor14, for
PT   treating inflammation e.g. rheumatoid arthritis -
XX
PS   Claim 2; Page 105-107; 112pp; English.
XX
CC   The invention provides a new human cytokine receptor desinated Zcytor14.
CC   Zcytor14 can be expressed by standard recombinant methodology. The
CC   encoding nucleic acid is useful for detecting the expression of a
CC   Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC   used to screen biological samples in vitro for the presence of Zcytor14.
CC   Proteins, polypeptides and peptides having Zcytor14 activity can be
CC   administered to a subject who lacks an adequate amount of this
CC   polypeptide, for treating inflammation and conditions such as rheumatoid
CC   arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC   antibodies) can be used to treat a subject who produces an excess of
CC   Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC   Zcytor14 to a subject. The present sequence represents a chimeric
CC   Zcytor14 protein.
XX
SQ   Sequence   705 AA;
```

```
  Query Match             99.6%;  Score 3699.5;  DB 22;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy    528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
```

```
RESULT 7
ABB95604
ID   ABB95604 standard; Protein; 705 AA.
XX
AC   ABB95604;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human angiogenesis related protein PRO20040 SEQ ID NO: 364.
```

XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95742.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 364; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 705 AA;

Query Match 99.6%; Score 3699.5; DB 23; Length 705;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

```
Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    480 ----------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy    528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
```

```
RESULT 8
ABB84998
ID   ABB84998 standard; Protein; 705 AA.
XX
AC   ABB84998;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO20040 protein sequence SEQ ID NO:364.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
PF   20-JUN-2001; 2001WO-US19692.
XX
PR   23-JUN-2000; 2000US-213637P.
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220664P.
PR   28-JUL-2000; 2000WO-US20710.
PR   02-AUG-2000; 2000US-222695P.
PR   17-AUG-2000; 2000US-0643657.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   07-SEP-2000; 2000US-230978P.
PR   18-SEP-2000; 2000US-0664610.
PR   18-SEP-2000; 2000US-0665350.
PR   24-OCT-2000; 2000US-242922P.
PR   08-NOV-2000; 2000US-0709238.
PR   08-NOV-2000; 2000WO-US30952.
PR   10-NOV-2000; 2000WO-US30873.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   22-JAN-2001; 2001US-0767609.
PR   28-FEB-2001; 2001US-0796498.
PR   28-FEB-2001; 2001WO-US06520.
PR   01-MAR-2001; 2001WO-US06666.
PR   09-MAR-2001; 2001US-0802706.
PR   14-MAR-2001; 2001US-0808689.
PR   22-MAR-2001; 2001US-0816744.
PR   05-APR-2001; 2001US-0828366.
PR   10-MAY-2001; 2001US-0854208.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001US-0866028.
PR   25-MAY-2001; 2001US-0866034.
PR   25-MAY-2001; 2001WO-US17092.
PR   30-MAY-2001; 2001US-0870574.
PR   30-MAY-2001; 2001WO-US17443.
PR   01-JUN-2001; 2001WO-US17800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-090516/12.
DR   N-PSDB; ABL88253.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal -
XX
PS   Claim 11; Fig 364; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC   e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC   degeneration, atherosclerosis, hypertension, arterial restenosis,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC   lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC   carcinoma) and wound healing. The PRO polynucleotides have applications
CC   in molecular biology, including use as hybridisation probes, and in
CC   chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC   probes used in the exemplification of the present invention.
XX
SQ   Sequence   705 AA;

  Query Match             99.6%;  Score 3699.5;  DB 23;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
```

```
RESULT 9
AAU98792
ID   AAU98792 standard; Protein; 705 AA.
XX
AC   AAU98792;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human interleukin 17 receptor like protein, splice variant protein #11.
XX
KW   Human; receptor; Interleukin 17 receptor-like protein; IL-17RL;
KW   chondroleukin; bone degradation; cartilage degradation; gene therapy;
KW   chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW   allergic skin immune response; organ transplant rejection; cytokine;
KW   osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;
KW   seronegative spondyloathropathy; bone morphogenetic protein;
KW   splice variant.
XX
OS   Homo sapiens.
XX
PN   WO200238764-A2.
XX
PD   16-MAY-2002.
XX
PF   13-NOV-2001; 2001WO-US43855.
XX
PR   10-NOV-2000; 2000US-247134P.
PR   23-FEB-2001; 2001US-271197P.
PR   12-OCT-2001; 2001US-328904P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Haudenschild D,  Rose L,  Moseley T,  Reddi AH;
XX
DR   WPI; 2002-508211/54.
DR   N-PSDB; ABK86558.
XX
PT   Interleukin-17 receptor-like polypeptide useful for the manufacture of
PT   a medicament to modulate cartilage or bone growth in a mammal  -
XX
PS   Claim 1; Page 87; 108pp; English.
XX
CC   The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC   polypeptide, with 85% or greater sequence identity to a polypeptide with
CC   a sequence appearing as AAU98781-AAU98792, where IL-17RL binds
CC   to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F.
CC   Also included are IL-17RL polynucleotides, antibodies, expression
CC   cassettes, transgenic host cells, a method of determining the
CC   aggressiveness of a prostate cancer cell, by determining the presence or
CC   absence in the cell of a group of IL-17RL (where the determination that
CC   the group is absent in the cell indicates that the cancer is more
CC   aggressive than a like cell in which the group is present) and a
CC   mammalian cell comprising a polynucleotide encoding an IL-17B antagonist,
CC   where the cell is selected from chondrocyte, synoviocyte, and mesenchymal
CC   stem cell. IL-17RL or the polynucleotide is useful for the manufacture of
CC   a medicament to modulate cartilage or bone growth in a mammal. The
CC   polynucleotide is useful for the manufacture of a medicament to restore
CC   androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for
CC   decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL
CC   is useful for inhibiting ossification or calcification in a mammal
CC   suffering from pathological ossification or calcification, for diagnosing
CC   a cartilage degenerative disorder in a mammal, for inhibiting the rate of
CC   proteoglycan synthesis by a chondrocyte in culture, and for the
CC   manufacture of a medicament to potentiate the activity of a bone
CC   morphogenetic protein in a mammal. An IL-17RL antagonist is useful
CC   for treating a bone or cartilage pathology such as a degenerative
CC   cartilage disorder selected from osteoarthritis, rheumatoid arthritis,
CC   relapsing polychondritis, seronegative spondyloathropathies, multiple
CC   sclerosis, allergic skin immune response and organ transplant rejection.
CC   IL-17RL is particularly a receptor for IL-17B (chondroleukin, a
CC   proinflammatory cytokine). The gene for IL-17RL is located on
CC   chromosome 3p25.3-3p24.1. The present sequence is the protein
CC   sequence encoded by a splice variant of IL-17RL.
XX
SQ   Sequence  705 AA;

  Query Match             99.4%;  Score 3695.5;  DB 23;  Length 705;
  Best Local Similarity   98.0%;  Pred. No. 0;
  Matches  691;  Conservative    1;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLQLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 10
AAU98781
ID   AAU98781 standard; Protein; 720 AA.
XX
AC   AAU98781;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human full length interleukin 17 receptor like protein, IL-17RL.
XX
KW   Human; receptor; Interleukin 17 receptor-like protein; IL-17RL;
KW   chondroleukin; bone degradation; cartilage degradation; gene therapy;
KW   chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW   allergic skin immune response; organ transplant rejection; cytokine;
KW   osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;
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KW   seronegative spondyloathropathy; bone morphogenetic protein.
XX
OS   Homo sapiens.
XX
PN   WO200238764-A2.
XX
PD   16-MAY-2002.
XX
PF   13-NOV-2001; 2001WO-US43855.
XX
PR   10-NOV-2000; 2000US-247134P.
PR   23-FEB-2001; 2001US-271197P.
PR   12-OCT-2001; 2001US-328904P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Haudenschild D,  Rose L,  Moseley T,  Reddi AH;
XX
DR   WPI; 2002-508211/54.
DR   N-PSDB; ABK86547.
XX
PT   Interleukin-17 receptor-like polypeptide useful for the manufacture of
PT   a medicament to modulate cartilage or bone growth in a mammal -
XX
PS   Claim 1; Fig 2; 108pp; English.
XX
CC   The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC   polypeptide, with 85% or greater sequence identity to a polypeptide with
CC   a sequence appearing as AAU98781-AAU98792, where IL-17RL binds
CC   to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F.
CC   Also included are IL-17RL polynucleotides, antibodies, expression
CC   cassettes, transgenic host cells, a method of determining the
CC   aggressiveness of a prostate cancer cell, by determining the presence or
CC   absence in the cell of a group of IL-17RL (where the determination that
CC   the group is absent in the cell indicates that the cancer is more
CC   aggressive than a like cell in which the group is present) and a
CC   mammalian cell comprising a polynucleotide encoding an IL-17B antagonist,
CC   where the cell is selected from chondrocyte, synoviocyte, and mesenchymal
CC   stem cell. IL-17RL or the polynucleotide is useful for the manufacture of
CC   a medicament to modulate cartilage or bone growth in a mammal. The
CC   polynucleotide is useful for the manufacture of a medicament to restore
CC   androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for
CC   decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL
CC   is useful for inhibiting ossification or calcification in a mammal
CC   suffering from pathological ossification or calcification, for diagnosing
CC   a cartilage degenerative disorder in a mammal, for inhibiting the rate of
CC   proteoglycan synthesis by a chondrocyte in culture, and for the
CC   manufacture of a medicament to potentiate the activity of a bone
CC   morphogenetic protein in a mammal. An IL-17RL antagonist is useful
CC   for treating a bone or cartilage pathology such as a degenerative
CC   cartilage disorder selected from osteoarthritis, rheumatoid arthritis,
CC   relapsing polychondritis, seronegative spondyloathropathies, multiple
CC   sclerosis, allergic skin immune response and organ transplant rejection.
CC   IL-17RL is particularly a receptor for IL-17B (chondroleukin, a
CC   proinflammatory cytokine). The gene for IL-17RL is located on
CC   chromosome 3p25.3-3p24.1. The present sequence is the full length
CC   sequence for IL-17RL.
XX
SQ   Sequence   720 AA;

  Query Match             98.3%;  Score 3654;  DB 23;  Length 720;
  Best Local Similarity   95.6%;  Pred. No. 0;
  Matches  688;  Conservative    0;  Mismatches    4;  Indels   28;  Gaps    2;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADLGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPCCLVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLP--------------ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 225
           ||||||||||||              ||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 240

Qy     226 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 300

Qy     286 WQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 WQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 360

Qy     346 LKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 405
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     361 LKGHPNLCVQVNSSEKLQLQECLRADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 420

Qy     406 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 465
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 480

Qy     466 ALSLILLLKKDHAK------------AAARGRAALLLYSADDSGFERLVGALASALCQL 512
           ||||||||||||||              ||||||||||||||||||||||||||||||||
Db     481 ALSLILLLKKDHAKGWLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQL 540

Qy     513 PLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 PLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 600

Qy     573 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 660

Qy     633 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 720


RESULT 11
AAB61885
ID   AAB61885 standard; Protein; 675 AA.
XX
AC   AAB61885;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Chimeric Zcytor14 protein #3.
XX
KW   Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW   antiinflammatory; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO200104304-A1.
XX
PD   18-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US18383.
XX
PR   07-JUL-1999;   99US-0348854.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Burkhead SK,  Pownder SL;
XX
DR   WPI; 2001-112618/12.
XX
PT   New polypeptide encoding a human cytokine receptor Zcytor14, for
PT   treating inflammation e.g. rheumatoid arthritis -
XX
PS   Claim 2; Page 107-109; 112pp; English.
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XX
CC   The invention provides a new human cytokine receptor desinated Zcytor14.
CC   Zcytor14 can be expressed by standard recombinant methodology. The
CC   encoding nucleic acid is useful for detecting the expression of a
CC   Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC   used to screen biological samples in vitro for the presence of Zcytor14.
CC   Proteins, polypeptides and peptides having Zcytor14 activity can be
CC   administered to a subject who lacks an adequate amount of this
CC   polypeptide, for treating inflammation and conditions such as rheumatoid
CC   arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC   antibodies) can be used to treat a subject who produces an excess of
CC   Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC   Zcytor14 to a subject. The present sequence represents a chimeric
CC   Zcytor14 protein.
XX
SQ   Sequence   675 AA;

  Query Match             97.0%;  Score 3604.5;  DB 22;  Length 675;
  Best Local Similarity   97.5%;  Pred. No. 0;
  Matches  675;  Conservative    0;  Mismatches    0;  Indels   17;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVD----------------VNSSE 343

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     344 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 403

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     404 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 463

Qy     481 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     464 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 523

Qy     541 QTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGS 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     524 QTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGS 583

Qy     601 YVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAL 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     584 YVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAL 643

Qy     661 QPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           ||||||||||||||||||||||||||||||||
Db     644 QPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 675


RESULT 12
AAB61883
ID   AAB61883 standard; Protein; 688 AA.
XX
AC   AAB61883;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Chimeric Zcytor14 protein #1.
XX
KW   Cytokine receptor; Zcytor14; human; inflammation; rheumatoid arthritis;
KW   antiinflammatory; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO200104304-A1.
XX
PD   18-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US18383.
XX
PR   07-JUL-1999;   99US-0348854.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Burkhead SK,  Pownder SL;
XX
DR   WPI; 2001-112618/12.
XX
PT   New polypeptide encoding a human cytokine receptor Zcytor14, for
PT   treating inflammation e.g. rheumatoid arthritis -
XX
PS   Claim 2; Page 102-104; 112pp; English.
XX
CC   The invention provides a new human cytokine receptor desinated Zcytor14.
CC   Zcytor14 can be expressed by standard recombinant methodology. The
CC   encoding nucleic acid is useful for detecting the expression of a
CC   Zcytor14 gene in a biological sample. Anti-Zcytor14 antibodies can be
CC   used to screen biological samples in vitro for the presence of Zcytor14.
CC   Proteins, polypeptides and peptides having Zcytor14 activity can be
CC   administered to a subject who lacks an adequate amount of this
CC   polypeptide, for treating inflammation and conditions such as rheumatoid
CC   arthritis. In contrast, Zcytor14 antagonists (e.g. anti-Zcytor14
CC   antibodies) can be used to treat a subject who produces an excess of
CC   Zcytor14. Zcytor14 nucleotide sequences can also be used to provide
CC   Zcytor14 to a subject. The present sequence represents a chimeric
CC   Zcytor14 protein.
XX
SQ   Sequence   688 AA;

  Query Match             96.6%;  Score 3588;  DB 22;  Length 688;
  Best Local Similarity   95.7%;  Pred. No. 0;
  Matches  675;  Conservative    0;  Mismatches    0;  Indels   30;  Gaps    2;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVD----------------VNSSE 343

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     344 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 403

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     404 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 463

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       |||||||||||||||||||||||||||||||||||||||||||||||||
Db     464 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 523

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     524 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 583

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     584 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 643

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     644 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 688


RESULT 13
AAU98791
ID   AAU98791 standard; Protein; 703 AA.
XX
AC   AAU98791;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human interleukin 17 receptor like protein, splice variant protein #10.
XX
KW   Human; receptor; Interleukin 17 receptor-like protein; IL-17RL;
KW   chondroleukin; bone degradation; cartilage degradation; gene therapy;
KW   chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW   allergic skin immune response; organ transplant rejection; cytokine;
KW   osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;
KW   seronegative spondyloathropathy; bone morphogenetic protein;
KW   splice variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 612
FT                   /note= "Encoded by TC"
XX
PN   WO200238764-A2.
XX
PD   16-MAY-2002.
XX
PF   13-NOV-2001; 2001WO-US43855.
XX
PR   10-NOV-2000; 2000US-247134P.
PR   23-FEB-2001; 2001US-271197P.
PR   12-OCT-2001; 2001US-328904P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Haudenschild D,  Rose L,  Moseley T,  Reddi AH;
XX
DR   WPI; 2002-508211/54.
DR   N-PSDB; ABK86557.
XX
PT   Interleukin-17 receptor-like polypeptide useful for the manufacture of
PT   a medicament to modulate cartilage or bone growth in a mammal  -
XX
PS   Claim 1; Page 85-86; 108pp; English.
XX
CC   The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC   polypeptide, with 85% or greater sequence identity to a polypeptide with
CC   a sequence appearing as AAU98781-AAU98792, where IL-17RL binds
CC   to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F.
CC   Also included are IL-17RL polynucleotides, antibodies, expression
CC   cassettes, transgenic host cells, a method of determining the
CC   aggressiveness of a prostate cancer cell, by determining the presence or
CC   absence in the cell of a group of IL-17RL (where the determination that
CC   the group is absent in the cell indicates that the cancer is more
CC   aggressive than a like cell in which the group is present) and a
CC   mammalian cell comprising a polynucleotide encoding an IL-17B antagonist,
CC   where the cell is selected from chondrocyte, synoviocyte, and mesenchymal
CC   stem cell. IL-17RL or the polynucleotide is useful for the manufacture of
CC   a medicament to modulate cartilage or bone growth in a mammal. The
CC   polynucleotide is useful for the manufacture of a medicament to restore
CC   androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for
CC   decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL
CC   is useful for inhibiting ossification or calcification in a mammal
CC   suffering from pathological ossification or calcification, for diagnosing
CC   a cartilage degenerative disorder in a mammal, for inhibiting the rate of
CC   proteoglycan synthesis by a chondrocyte in culture, and for the
CC   manufacture of a medicament to potentiate the activity of a bone
CC   morphogenetic protein in a mammal. An IL-17RL antagonist is useful
CC   for treating a bone or cartilage pathology such as a degenerative
CC   cartilage disorder selected from osteoarthritis, rheumatoid arthritis,
CC   relapsing polychondritis, seronegative spondyloathropathies, multiple
CC   sclerosis, allergic skin immune response and organ transplant rejection.
CC   IL-17RL is particularly a receptor for IL-17B (chondroleukin, a
CC   proinflammatory cytokine). The gene for IL-17RL is located on
CC   chromosome 3p25.3-3p24.1. The present sequence is the protein
CC   sequence encoded by a splice variant of IL-17RL.
XX
SQ   Sequence   703 AA;

  Query Match             96.0%;  Score 3566.5;  DB 23;  Length 703;
  Best Local Similarity   93.6%;  Pred. No. 5e-317;
  Matches  674;  Conservative    1;  Mismatches    0;  Indels   45;  Gaps    3;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLP----------------ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 225
           ||||||||||||                ||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 240

Qy     226 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 285
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 300

Qy     286 WQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 345
           ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 WQAARLQLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVD------- 353

Qy     346 LKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 405
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 ----------VNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 403

Qy     406 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     404 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 463

Qy     466 ALSLILLLKKDHAK-------------AAARGRAALLLYSADDSGFERLVGALASALCQL 512
           |||||||||||||              ||||||||||||||||||||||||||||||||||
Db     464 ALSLILLLKKDHAKGWLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQL 523
```

```
Qy     513 PLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     524 PLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 583

Qy     573 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     584 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 643

Qy     633 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     644 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 703
```

RESULT 14
AAU11353
ID AAU11353 standard; Protein; 703 AA.
XX
AC AAU11353;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX cytokine receptor subunit 7 (DCRS7) polypeptide.
XX
KW Human; DNAX cytokine receptor subunit 7; DCRS7; phosphate labelling;
KW gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 684
FT /label= Thr
FT /note= "Encoded by ACN"
XX
PN WO200190358-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US16767.
XX
PR 24-MAY-2000; 2000US-206862P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM;
XX
DR WPI; 2002-106198/14.
DR N-PSDB; AAS18130.
XX
PT Isolated antigenic human or mouse DNAX receptor subunit-like
PT polypeptide useful for detecting antibodies generated in response to
PT presence of increased protein levels or immunological disorders -
XX
PS Disclosure; Page 15; 148pp; English.
XX
CC The invention relates to primate and rodent DNAX cytokine receptor
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC receptors, or their portions may be useful as phosphate labelling enzymes
CC to label general or specific substrates. The subunits may also be
CC functional immunogens to elicit recognising antibodies, or antigens
CC capable of binding antibodies. A combination, e.g., including a DCRS can
CC be used as an immunogen for the production of antisera or antibodies
CC capable of distinguishing between other cytokine receptor family members.
CC A purified DCRS can also be used as a reagent to detect antibodies
CC generated in response to the presence of elevated levels of expression,
CC or immunological disorders which lead to antibody production to the
CC endogenous receptor. This sequence represents the human DCRS7
CC polypeptide.
XX
SQ Sequence 703 AA;

Query Match 95.1%; Score 3535.5; DB 23; Length 703;
Best Local Similarity 92.9%; Pred. No. 3.5e-314;

Matches 669; Conservative 1; Mismatches 5; Indels 45; Gaps 3;

```
Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           |||||||||||||||  :||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSQWILSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADLGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLP--------------ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 225
           ||||||||||||              ||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 240

Qy     226 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 300

Qy     286 WQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 345
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 WQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVD------- 353

Qy     346 LKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 405
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     354 ----------VNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 403

Qy     406 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     404 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 463

Qy     466 ALSLILLLKKDHAK-------------AAARGRAALLLYSADDSGFERLVGALASALCQL 512
           ||||||||||||||              ||||||||||||||||||||||||||||||||||
Db     464 ALSLILLLKKDHAKGWLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQL 523

Qy     513 PLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     524 PLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 583

Qy     573 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     584 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 643

Qy     633 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db     644 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGXSAPGRGVGPGAGPGAGDGT 703
```

RESULT 15
AAU98790
ID AAU98790 standard; Protein; 693 AA.
XX
AC AAU98790;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human interleukin 17 receptor like protein, splice variant protein #9.
XX
KW Human; receptor; Interleukin 17 receptor-like protein; IL-17RL;
KW chondroleukin; bone degradation; cartilage degradation; gene therapy;
KW chromosome 3p25.3-3p24.1; rheumatoid arthritis; multiple sclerosis;
KW allergic skin immune response; organ transplant rejection; cytokine;
KW osteopathic; antirheumatic; antiarthritic; relapsing polychondritis;
KW seronegative spondyloathropathy; bone morphogenetic protein;
KW splice variant.
XX
OS Homo sapiens.
XX
PN WO200238764-A2.
XX

PD 16-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US43855.
XX
PR 10-NOV-2000; 2000US-247134P.
PR 23-FEB-2001; 2001US-271197P.
PR 12-OCT-2001; 2001US-328904P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Haudenschild D, Rose L, Moseley T, Reddi AH;
XX
DR WPI; 2002-508211/54.
DR N-PSDB; ABK86556.
XX
PT Interleukin-17 receptor-like polypeptide useful for the manufacture of
PT a medicament to modulate cartilage or bone growth in a mammal -
XX
PS Claim 1; Page 84; 108pp; English.
XX
CC The invention relates to an interleukin-17 receptor-like (IL-17RL)
CC polypeptide, with 85% or greater sequence identity to a polypeptide with
CC a sequence appearing as AAU98781-AAU98792, where IL-17RL binds
CC to an IL-17 selected from IL-17A, IL-17B, IL-17C, IL-17E and IL-17F.
CC Also included are IL-17RL polynucleotides, antibodies, expression
CC cassettes, transgenic host cells, a method of determining the
CC aggressiveness of a prostate cancer cell, by determining the presence or
CC absence in the cell of a group of IL-17RL (where the determination that
CC the group is absent in the cell indicates that the cancer is more
CC aggressive than a like cell in which the group is present) and a
CC mammalian cell comprising a polynucleotide encoding an IL-17B antagonist,
CC where the cell is selected from chondrocyte, synoviocyte, and mesenchymal
CC stem cell. IL-17RL or the polynucleotide is useful for the manufacture of
CC a medicament to modulate cartilage or bone growth in a mammal. The
CC polynucleotide is useful for the manufacture of a medicament to restore
CC androgen-responsiveness to a prostate cancer cell. IL-17RL is useful for
CC decreasing catabolic activity in bone or cartilage in a mammal. IL-17RL
CC is useful for inhibiting ossification or calcification in a mammal
CC suffering from pathological ossification or calcification, for diagnosing
CC a cartilage degenerative disorder in a mammal, for inhibiting the rate of
CC proteoglycan synthesis by a chondrocyte in culture, and for the
CC manufacture of a medicament to potentiate the activity of a bone
CC morphogenetic protein in a mammal. An IL-17RL antagonist is useful
CC for treating a bone or cartilage pathology such as a degenerative
CC cartilage disorder selected from osteoarthritis, rheumatoid arthritis,
CC relapsing polychondritis, seronegative spondyloathropathies, multiple
CC sclerosis, allergic skin immune response and organ transplant rejection.
CC IL-17RL is particularly a receptor for IL-17B (chondroleukin, a
CC proinflammatory cytokine). The gene for IL-17RL is located on
CC chromosome 3p25.3-3p24.1. The present sequence is the protein
CC sequence encoded by a splice variant of IL-17RL.
XX
SQ Sequence 693 AA;

Query Match 94.5%; Score 3510.5; DB 23; Length 693;
Best Local Similarity 92.2%; Pred. No. 6.7e-312;
Matches 664; Conservative 1; Mismatches 0; Indels 55; Gaps 3;

```
Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy    181 YEKELNHTQQLP--------------ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 225
          ||||||||||||              ||||||||||||||||||||||||||||||||
Db    181 YEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 240

Qy    226 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 300

Qy    286 WQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 345
          ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 WQAARLQLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 360

Qy    346 LKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 LKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 420

Qy    406 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 PSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAA 480

Qy    466 ALSLILLLKKDHAK------------AAARGRAALLLYSADDSGFERLVGALASALCQL 512
          ||||||||||||||              ||||||||||||||||||||||||||||||
Db    481 ALSLILLLKKDHAKGWLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALC-- 538

Qy    513 PLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 572
                                  ||||||||||||||||||||||||||||||||
Db    539 ------------------------QRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGP 573

Qy    573 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLP 633

Qy    633 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 DFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 693
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Search completed: February 24, 2003, 09:22:33
Job time : 42 secs

GenCore version 5.1.3


OM protein - protein search, using sw model

Run on: February 24, 2003, 09:21:11 ; Search time 18 Seconds
(without alignments)
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Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLSLALGRSPVVLS.....TPAPGRGVGPGAGPGAGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 326.5 | 8.8 | 617 | 4 | US-09-188-930-303 | Sequence 303, App |
| 2 | 174 | 4.7 | 866 | 2 | US-08-620-694A-10 | Sequence 10, Appl |
| 3 | 174 | 4.7 | 866 | 3 | US-09-022-255-10 | Sequence 10, Appl |
| 4 | 174 | 4.7 | 866 | 3 | US-09-022-696-10 | Sequence 10, Appl |
| 5 | 174 | 4.7 | 866 | 3 | US-08-978-773-4 | Sequence 4, Appli |
| 6 | 174 | 4.7 | 866 | 3 | US-09-022-253-10 | Sequence 10, Appl |
| 7 | 174 | 4.7 | 866 | 3 | US-09-022-260-10 | Sequence 10, Appl |
| 8 | 174 | 4.7 | 866 | 4 | US-09-022-259-10 | Sequence 10, Appl |
| 9 | 174 | 4.7 | 866 | 4 | US-09-022-257-10 | Sequence 10, Appl |
| 10 | 165 | 4.4 | 864 | 2 | US-08-620-694A-2 | Sequence 2, Appli |
| 11 | 165 | 4.4 | 864 | 3 | US-09-022-255-2 | Sequence 2, Appli |
| 12 | 165 | 4.4 | 864 | 3 | US-09-022-696-2 | Sequence 2, Appli |
| 13 | 165 | 4.4 | 864 | 3 | US-08-978-773-2 | Sequence 2, Appli |
| 14 | 165 | 4.4 | 864 | 3 | US-09-022-253-2 | Sequence 2, Appli |
| 15 | 165 | 4.4 | 864 | 3 | US-09-022-260-2 | Sequence 2, Appli |
| 16 | 165 | 4.4 | 864 | 4 | US-09-022-259-2 | Sequence 2, Appli |
| 17 | 165 | 4.4 | 864 | 4 | US-09-022-257-2 | Sequence 2, Appli |
| 18 | 162 | 4.4 | 330 | 4 | US-09-188-930-125 | Sequence 125, App |
| 19 | 116.5 | 3.1 | 1711 | 2 | US-08-342-930-2 | Sequence 2, Appli |
| 20 | 112.5 | 3.0 | 1208 | 4 | US-09-463-702A-2 | Sequence 2, Appli |
| 21 | 108 | 2.9 | 2629 | 2 | US-08-751-189-4 | Sequence 4, Appli |
| 22 | 108 | 2.9 | 2629 | 2 | US-09-060-836-4 | Sequence 4, Appli |
| 23 | 108 | 2.9 | 2629 | 4 | US-09-184-445-4 | Sequence 4, Appli |
| 24 | 107 | 2.9 | 4928 | 4 | US-09-036-987A-5 | Sequence 5, Appli |
| 25 | 107 | 2.9 | 4928 | 4 | US-09-370-700-5 | Sequence 5, Appli |
| 26 | 106 | 2.9 | 449 | 3 | US-08-897-236-23 | Sequence 23, Appl |
| 27 | 103.5 | 2.8 | 3739 | 3 | US-09-320-878-2 | Sequence 2, Appli |
| 28 | 101.5 | 2.7 | 469 | 3 | US-08-753-007A-8 | Sequence 8, Appli |
| 29 | 101.5 | 2.7 | 469 | 4 | US-09-398-496-8 | Sequence 8, Appli |
| 30 | 100 | 2.7 | 954 | 2 | US-08-749-169A-3 | Sequence 3, Appli |
| 31 | 100 | 2.7 | 954 | 2 | US-09-130-032A-3 | Sequence 3, Appli |
| 32 | 99 | 2.7 | 3724 | 2 | US-08-804-227C-10 | Sequence 10, Appl |
| 33 | 99 | 2.7 | 3724 | 2 | US-08-804-198-4 | Sequence 4, Appli |
| 34 | 98 | 2.6 | 623 | 1 | US-08-653-740-7 | Sequence 7, Appli |
| 35 | 98 | 2.6 | 623 | 2 | US-09-073-594-7 | Sequence 7, Appli |
| 36 | 98 | 2.6 | 623 | 3 | US-09-275-925-7 | Sequence 7, Appli |
| 37 | 98 | 2.6 | 2205 | 1 | US-08-093-453B-2 | Sequence 2, Appli |
| 38 | 97.5 | 2.6 | 647 | 3 | US-08-753-007A-32 | Sequence 32, Appl |
| 39 | 97.5 | 2.6 | 647 | 4 | US-09-398-496-32 | Sequence 32, Appl |
| 40 | 97.5 | 2.6 | 3739 | 4 | US-09-105-537-33 | Sequence 33, Appl |
| 41 | 97.5 | 2.6 | 11877 | 4 | US-09-105-537-6 | Sequence 6, Appli |
| 42 | 97 | 2.6 | 1326 | 4 | US-09-147-236-5 | Sequence 5, Appli |
| 43 | 96.5 | 2.6 | 579 | 4 | US-09-171-710-6 | Sequence 6, Appli |
| 44 | 96 | 2.6 | 405 | 2 | US-08-483-151-4 | Sequence 4, Appli |
| 45 | 96 | 2.6 | 1843 | 4 | US-09-413-814-50 | Sequence 50, Appl |

ALIGNMENTS

RESULT 1
US-09-188-930-303
; Sequence 303, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-303

Query Match 8.8%; Score 326.5; DB 4; Length 617;
Best Local Similarity 26.7%; Pred. No. 1.4e-22;
Matches 132; Conservative 56; Mismatches 184; Indels 123; Gaps 19;

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Qy    237 KNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAH-QNLWQAAR----- 290
          | ::|   : | :  |:||:||:   |: |:||  |||:  | |:  : ||: |
Db    183 KIVSGGHTVDLPYEFLLPCMCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWQSIRFTDYS 242

Qy    291 -----LRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 345
               :  |||:       | |  ||:||||     ||: |       | | :   : :
Db    243 QHNQMVMALTLR-------CPLKLEASLCWRQDPLTPCETL------PNATAQESEGWYI 289

Qy    346 LKG---HPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGC 402
          |:    || || :  | |     ||      | |    : ::|:  |        |  |
Db    290 LENVDLHPQLCFKF-SFENSSHVEC--PHQSGSLPSWTVSMDTQAQQ-----LTLHFSSR 341

Qy    403 TSLPSKASTRAARLG---------------------EYLLQDLQSGQCLQLWDDDLGAL 440
          |     |:     ||                     : ::  |:   |: :|  |:
Db    342 TYATFSAAWSDPGLGPDTPMPPVYSISQTQGSVPVTLDLIIPFLRQENCILVWRSDVHFA 401

Qy    441 W---ACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSG 497
          |    || |                   |     |||:   :  : | |  |||::||
Db    402 WKHVLCPDD-----------------APYPTQLLLR---SLGSGRTRPVLLLHAADSEA 440

Qy    498 FERLVGALASALCQLPLRVA--------VDLWSRRELSAQGPVAWFHAQRRQTLQEGGVV 549
          |||||||        || |        ||||    ::  ||: |  | | :  :| | |
Db    441 QRRLVGALAEL-----LRTALGGGRDVIVDLWEGTHVARIGPLPWLWAARERVAREQGTV 495
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Qy     550 VLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRL 609
           :||::               :||      |   |||  :|       ||   : | | ||
Db     496 LLLWN-------------CAGPSTACSGDPQAASLRTLL-----CAAPRPLLLAYFSRL 536

Qy     610 LHPDAVPALFRTVPVFTLPSQLPDFLGALQ-QPRAPRSG--------RLQERAEQVS-RA 659
             :|   | :| : |   ||  | ||  ||     |          |: | ||
Db     537 CAKGDIPRPLRALPRYRLLRDLPRLLRALDAQPATLASSWSHLGAKRCLKNRLEQCHLLE 596

Qy     660 LQPALDSYFHPPGTP 674
           |: | | |     :|
Db     597 LEAAKDDYQGSTNSP 611


RESULT 2
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 5869286el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694A
;      FILING DATE:  21 MARCH 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-620-694A-10

  Query Match             4.7%;  Score 174;  DB 2;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;

Qy     237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
           :|||   |: : :     ||   || |   |: | |: |:              : ||
Db      66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy     272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
           :|    |    | |   |:       |   :::|          ||         | ||

Db     125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy     322 PCQP----LVPPLSWENVTVDKVLEPPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
           |       |||      : |      | :       ||: |:   : :|::   || :|
Db     173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy     374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
                 :| | |         :|   |       :|       | |  |:          |
Db     228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy     422 QDLQS------------GQCLQLWDDDL--GALWACP------------MDKYIHKRWAL 455
           ::|:              ||   :| |   | :||           |  :::  | :
Db     271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy     456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492
             :: ||  : : ||: :                  |   ||       : |  .::||
Db     326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy     493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
           ||   :  :|   |   |       ||:||   : :|  | : |   |::: ::    :::
Db     386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy     552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
           | | |  |   :|    : | ||          ||    | | |::: :|||| :    |:||
Db     446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy     603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
             |  :     || ||   | : |  :  :    :|     : ||:  |  ::|
Db     501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy     663 ALDSYFHPPG 672
           |:|   ||
Db     556 --DNYLRSPG 563


RESULT 3
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072033el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,255
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/620,694
;      FILING DATE:  21 MARCH 1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
```

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-255-10

  Query Match             4.7%;  Score 174;  DB 3;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;

Qy     237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
           :|||   |: : :     ||   || |   |: | |: |:              : ||
Db      66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy     272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
           :|    |    | |   |:       |   :::|           ||          | ||
Db     125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy     322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
           |       |||      : |      | :       ||: |:   : :|::   || :|
Db     173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy     374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
                :| |  |        :|    |       :|      | |  |:          |
Db     228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy     422 QDLQS------------GQCLQLWDDDL--GALWACP------------MDKYIHKRWAL 455
           ::|:                ||   :| |   |  :||            |  :::  | :
Db     271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy     456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492
             :: ||  : : ||: :                  |   ||       : |   ::||
Db     326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy     493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
           ||   :  :|   |   |      ||:||   : :|  | : |   |::: ::    :::
Db     386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy     552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
           | | |  |   :|    : | ||       ||    | | |::: :|||| :    |:||
Db     446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy     603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
             |  :     || ||   | : |  :  :    :|     : ||:  |  ::|
Db     501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy     663 ALDSYFHPPG 672
             |:|   ||
Db     556 --DNYLRSPG 563


RESULT 4
US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072037el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,696
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-696-10

  Query Match             4.7%;  Score 174;  DB 3;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;

Qy     237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
           :|||   |: : :     ||   || |   |: | |: |:              : ||
Db      66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy     272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
           :|    |    | |   |:       |   :::|           ||          | ||
Db     125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy     322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
           |       |||      : |      | :       ||: |:   : :|::   || :|
Db     173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy     374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
                :| |  |        :|    |       :|      | |  |:          |
Db     228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy     422 QDLQS------------GQCLQLWDDDL--GALWACP------------MDKYIHKRWAL 455
           ::|:                ||   :| |   |  :||            |  :::  | :
Db     271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy     456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492
             :: ||  : : ||: :                  |   ||       : |   ::||
Db     326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy     493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
           ||   :  :|   |   |      ||:||   : :|  | : |   |::: ::    :::
Db     386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy     552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
           | | |  |   :|    : | ||       ||    | | |::: :|||| :    |:||
Db     446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy     603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
             |  :     || ||   | : |  :  :    :|     : ||:  |  ::|
Db     501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy     663 ALDSYFHPPG 672
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Db    556 --DNYLRSPG 563


RESULT 5
US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906
;  GENERAL INFORMATION:
;    APPLICANT:  Troutt, Anthony
;    TITLE OF INVENTION:  Method of Regulating Nitric Oxide Production
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple PowerMacintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for PowerMacintosh, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,773
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 60/052,525
;      FILING DATE:  27 NOVEMBER 1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2623-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-773-4

  Query Match             4.7%;  Score 174;  DB 3;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;

Qy    237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS--------------VRTN-- 271
          :|||   |: : :     ||   || |   |: | |: |:               : ||
Db     66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy    272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
          :|    |    | |   |:       |  :::|          ||         | ||
Db    125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy    322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
          |       |||      : |      | :       ||: |:   : :|::   || :|
Db    173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy    374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
                :| |  |        :|   |      :|      | |  |:         |
Db    228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy    422 QDLQS------------GQCLQLWDDDL--GALWACP-----------MDKYIHKRWAL 455
          ::|:                ||   :| |   |  :||          |  :::  | :
Db    271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy    456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492
            :: ||  : : ||: :                  |   ||       : |   ::||
Db    326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy    493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
          ||   : :|   |   |      ||:||   : :|  | : |   |::: ::    :::
Db    386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy    552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
          | | |  |   :|    : | ||       ||    | | |::: :|||| :    |:||
Db    446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy    603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
              |:      || ||  | : |  :  :    :|     : ||:  |  ::|
Db    501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy    663 ALDSYFHPPG 672
            |:|   ||
Db    556 --DNYLRSPG 563


RESULT 6
US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6096305el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,253
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694
;      FILING DATE:  21-MARCH-1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-253-10

  Query Match             4.7%;  Score 174;  DB 3;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;
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```
Qy     237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
           :|||   |: : :     ||   || |   |: | |: |:              : ||
Db      66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy     272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
           :|    |    | |   |:       |   :::|           ||         | ||
Db     125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy     322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
           |       |||      : |      | :       ||: |:   : :|::   || :|
Db     173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy     374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
                :| |  |        :|   |      :|      | |  |:          |
Db     228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy     422 QDLQS-----------GQCLQLWDDDL--GALWACP-----------MDKYIHKRWAL 455
           ::|:              ||   :| |   |  :||           |  :::  | :
Db     271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy     456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492
             :: ||  : : ||: :                  |   ||       : |   ::||
Db     326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy     493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
           ||   :  :|   |   |      ||:||   : :|  | : |   |::: ::    :::
Db     386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy     552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
           | | |  |   :|    : | ||       ||    | | |::: :|||| :    |:||
Db     446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy     603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
             |  :     || ||   | : |  :  :    :|     : ||:  |  ::|
Db     501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy     663 ALDSYFHPPG 672
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Db     556 --DNYLRSPG 563


RESULT 7
US-09-022-260-10
; Sequence 10, Application US/09022260
; Patent No. 6100235
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6100235el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,260
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-260-10

  Query Match             4.7%;  Score 174;  DB 3;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;

Qy     237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
           :|||   |: : :     ||   || |   |: | |: |:              : ||
Db      66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy     272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
           :|    |    | |   |:       |   :::|           ||         | ||
Db     125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy     322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
           |       |||      : |      | :       ||: |:   : :|::   || :|
Db     173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy     374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
                :| |  |        :|   |      :|      | |  |:          |
Db     228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy     422 QDLQS-----------GQCLQLWDDDL--GALWACP-----------MDKYIHKRWAL 455
           ::|:              ||   :| |   |  :||           |  :::  | :
Db     271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy     456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492
             :: ||  : : ||: :                  |   ||       : |   ::||
Db     326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy     493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
           ||   :  :|   |   |      ||:||   : :|  | : |   |::: ::    :::
Db     386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy     552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
           | | |  |   :|    : | ||       ||    | | |::: :|||| :    |:||
Db     446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy     603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
             |  :     || ||   | : |  :  :    :|     : ||:  |  ::|
Db     501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy     663 ALDSYFHPPG 672
             |:|   ||
Db     556 --DNYLRSPG 563


RESULT 8
US-09-022-259-10
; Sequence 10, Application US/09022259
; Patent No. 6191104
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6191104el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,259
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-259-10

  Query Match             4.7%;  Score 174;  DB 4;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;

Qy     237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
           :|||   |: : :     ||   || |   |: | |: |:                : ||
Db      66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy     272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
           :|    |    | |   |:       |   :::|           ||          | ||
Db     125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy     322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
           |       |||      : |      | :       ||: |:   : :|::   || :|
Db     173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy     374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
               :| |  |       :|   |     :|     | |  |:          |
Db     228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy     422 QDLQS------------GQCLQLWDDDL--GALWACP-----------MDKYIHKRWAL 455
           ::|:              ||   :| |   |  :||           |  :::  | :
Db     271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy     456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492
             :: ||  : : ||: :                  |   ||       : |   ::||
Db     326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy     493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
           ||   :  :|   |  |     ||:||   : :|  | : |   |::: ::     :::
Db     386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy     552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
           | | |  |   :|    : | ||       ||    | | |::: :|||| :    |:||
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Db     446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy     603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
             |  :     || ||   | : |  :  :    :|     : ||:  |  ::|
Db     501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy     663 ALDSYFHPPG 672
             |:|   ||
Db     556 --DNYLRSPG 563


RESULT 9
US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6197525el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,257
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 866 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-257-10

  Query Match             4.7%;  Score 174;  DB 4;  Length 866;
  Best Local Similarity   21.6%;  Pred. No. 1.1e-07;
  Matches  119;  Conservative   76;  Mismatches  189;  Indels  166;  Gaps   32;

Qy     237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
           :|||   |: : :     ||   || |   |: | |: |:                : ||
Db      66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy     272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
           :|    |    | |   |:       |   :::|           ||          | ||
Db     125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy     322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
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Db    173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy    374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421

Db    228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy    422 QDLQS------------GQCLQLWDDDL--GALWACP------------MDKYIHKRWAL 455

Db    271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy    456 VWLACLLFAAALSLILLLK----------------KDHAKAA------ARGRAALLLYS 492

Db    326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYS 385

Qy    493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551

Db    386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy    552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602

Db    446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy    603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662

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Qy    663 ALDSYFHPPG 672

Db    556 --DNYLRSPG 563


RESULT 10
US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 5869286el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694A
;      FILING DATE:  21 MARCH 1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)

;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-620-694A-2

  Query Match             4.4%;  Score 165;  DB 2;  Length 864;
  Best Local Similarity   19.8%;  Pred. No. 7.7e-07;
  Matches  123;  Conservative   79;  Mismatches  209;  Indels  210;  Gaps   31;

Qy    192 PALPW----LNVSADGDNVHLVLN----VSEEQHFGLSLYWNQVQGPP--KPRW--HKNL 239

Db     14 PALGWLLLLLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDDSWIHPKNL 68

Qy    240 T--GPQIITLN-------HTDLVPCLCIQVWPLEPDS--------------VRTN--IC- 273

Db     69 TPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNERLCV 127

Qy    274 --PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEA------ALCWRAPGGDP--- 322

Db    128 KFQFLSMLQHHRKRWR------FSFSHFVVD-----PGQEYEVTVHHLPKPIPDGDPNHK 176

Qy    323 --------CQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374

Db    177 SKIIFVPDCEDSKMKMTTSCVSSGSLWD-------PNITVETLDTQHLRVDFTLWNEST- 228

Qy    375 PLKDDVLLLETRGPQDNRSLCALEPSGCTSL------PSKASTRAARLGEYLLQDLQSGQ 428

Db    229 PYQ---VLLESFSDSENHS--------CFDVVKQIFAPRQEEFHQRANVTFTLSKFH--- 274

Qy    429 CLQLWDDDLGALWAC-----------------------------------PMDKYIHKR 452

Db    275 -----------WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321

Qy    453 WA---LVWLACLLFAAALSLILLLK----------------------KDHAKAAARGRA 486

Db    322 WVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPRK 381

Qy    487 ALLLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQE 545

Db    382 VWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVES 441

Qy    546 GGVVVLLFSPG--------------AVAL-CSEWLQDGVSGPGAHGPHDAFRASLSCVLP 590

Db    442 NSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPAG----------DLFTAAMNMILP 491

Qy    591 DFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQ 650

Db    492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEMFEPGRMH 551

Qy    651 ERAEQVSRALQPALDSYFHPP 671

Db    552 HVRELTG-------DNYLQSP 565


RESULT 11
US-09-022-255-2
; Sequence 2, Application US/09022255
; Patent No. 6072033
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072033el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
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;       ZIP:  98101
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Apple Power Macintosh
;       OPERATING SYSTEM:  Apple Operating System 7.5.5
;       SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/022,255
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/620,694
;       FILING DATE:  21 MARCH 1996
;       APPLICATION NUMBER:  USSN 08/538,765
;       FILING DATE:  7 AUGUST 1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  USSN 08/410,535
;       FILING DATE:  23 MARCH 1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Perkins, Patricia Anne
;       REGISTRATION NUMBER:  34,695
;       REFERENCE/DOCKET NUMBER:  2617-B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206)587-0430
;       TELEFAX:  (206)
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;      LENGTH: 864 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-022-255-2

  Query Match             4.4%;  Score 165;  DB 3;  Length 864;
  Best Local Similarity  19.8%;  Pred. No. 7.7e-07;
  Matches  123;  Conservative   79;  Mismatches  209;  Indels  210;  Gaps   31;

Qy     192 PALPW----LNVSADGDNVHLVLN----VSEEQHFGLSLYWNQVQGPP--KPRW--HKNL 239
           |||  |    |||  |  |     :|:    |  ::  |||    :|:          |   |||
Db      14 PALGWLLLLLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDDSWIHPKNL 68

Qy     240 T--GPQIITLN-------HTDLVPCLCIQVWPLEPDS--------------VRTN--IC- 273
           |   |: |  :|        | :||| | :: | |: |:                : ||  :|
Db      69 TPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNERLCV 127

Qy     274 --PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEA------ALCWRAPGGDP--- 322
             |    : |:  |:        :   :::|     | :         |    | |||
Db     128 KFQFLSMLQHHRKRWR------FSFSHFVVD-----PGQEYEVTVHHLPKPIPDGDPNHK 176

Qy     323 --------CQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
                   |:     ::   |:   : :        ||: |:   :: |::   || :|
Db     177 SKIIFVPDCEDSKMKMTTSCVSSGSLWD-------PNITVETLDTQHLRVDFTLWNEST- 228

Qy     375 PLKDDVLLLETRGPQDNRSLCALEPSGCTSL------PSKASTRAARLGEYLLQDLQSGQ 428
           | :   :|||:    :| |        |  :      | :           : |
Db     229 PYQ---VLLESFSDSENHS--------CFDVVKQIFAPRQEEFHQRANVTFTLSKFH--- 274

Qy     429 CLQLWDDDLGALWAC-----------------------------------PMDKYIHKR 452
                   | |                                       |:  ||
Db     275 -----------WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321

Qy     453 WA---LVWLACLLFAAALSLILLLK----------------------KDHAKAAARGRA 486
           |    :  :| ||  : : ||: :                       |      | |
Db     322 WVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPRK 381

Qy     487 ALLLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQE 545
             ::||||   :  :|   |  |       ||:||   : :|  | : |   |::: ::
Db     382 VWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVES 441

Qy     546 GGVVVLLFSPG-------------AVAL-CSEWLQDGVSGPGAHGPHDAFRASLSCVLP 590
             :::| | |              || | |  |  |          | | |::: :||
Db     442 NSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPAG----------DLFTAAMNMILP 491
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Qy     591 DFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQ 650
           || :    |:||   |  :     || ||     : | :  :    :|        ||:
Db     492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEMFEPGRMH 551

Qy     651 ERAEQVSRALQPALDSYFHPP 671
             |         |:|   |
Db     552 HVRELTG-------DNYLQSP 565


RESULT 12
US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6072037el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,696
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-696-2

  Query Match             4.4%;  Score 165;  DB 3;  Length 864;
  Best Local Similarity  19.8%;  Pred. No. 7.7e-07;
  Matches  123;  Conservative   79;  Mismatches  209;  Indels  210;  Gaps   31;

Qy     192 PALPW----LNVSADGDNVHLVLN----VSEEQHFGLSLYWNQVQGPP--KPRW--HKNL 239
           |||  |    |||  |  |     :|:    |  ::  |||    :|:          |   |||
Db      14 PALGWLLLLLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDDSWIHPKNL 68

Qy     240 T--GPQIITLN-------HTDLVPCLCIQVWPLEPDS--------------VRTN--IC- 273
           |   |: |  :|        | :||| | :: | |: |:                : ||  :|
Db      69 TPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNERLCV 127

Qy     274 --PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEA------ALCWRAPGGDP--- 322
             |    : |:  |:        :   :::|     | :         |    | |||
Db     128 KFQFLSMLQHHRKRWR------FSFSHFVVD-----PGQEYEVTVHHLPKPIPDGDPNHK 176
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Qy    323 --------CQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
Db    177 SKIIFVPDCEDSKMKMTTSCVSSGSLWD-------PNITVETLDTQHLRVDFTLWNEST- 228

Qy    375 PLKDDVLLLETRGPQDNRSLCALEPSGCTSL------PSKASTRAARLGEYLLQDLQSGQ 428
Db    229 PYQ---VLLESFSDSENHS--------CFDVVKQIFAPRQEEFHQRANVTFTLSKFH--- 274

Qy    429 CLQLWDDDLGALWAC-----------------------------------PMDKYIHKR 452
Db    275 -----------WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321

Qy    453 WA---LVWLACLLFAAALSLILLLK----------------------KDHAKAAARGRA 486
Db    322 WVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPRK 381

Qy    487 ALLLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQE 545
Db    382 VWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVES 441

Qy    546 GGVVVLLFSPG--------------AVAL-CSEWLQDGVSGPGAHGPHDAFRASLSCVLP 590
Db    442 NSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPAG----------DLFTAAMNMILP 491

Qy    591 DFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQ 650
Db    492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEMFEPGRMH 551

Qy    651 ERAEQVSRALQPALDSYFHPP 671
Db    552 HVRELTG-------DNYLQSP 565
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RESULT 13
US-08-978-773-2
; Sequence 2, Application US/08978773
; Patent No. 6083906
;  GENERAL INFORMATION:
;    APPLICANT:  Troutt, Anthony
;    TITLE OF INVENTION:  Method of Regulating Nitric Oxide Production
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple PowerMacintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for PowerMacintosh, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,773
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 60/052,525
;      FILING DATE:  27 NOVEMBER 1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,693
;      REFERENCE/DOCKET NUMBER:  2623-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-978-773-2

  Query Match             4.4%;  Score 165;  DB 3;  Length 864;
  Best Local Similarity   19.8%;  Pred. No. 7.7e-07;
  Matches  123;  Conservative   79;  Mismatches  209;  Indels  210;  Gaps   31;

Qy    192 PALPW----LNVSADGDNVHLVLN----VSEEQHFGLSLYWNQVQGPP--KPRW--HKNL 239
Db     14 PALGWLLLLLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDDSWIHPKNL 68

Qy    240 T--GPQIITLN-------HTDLVPCLCIQVWPLEPDS-------------VRTN--IC- 273
Db     69 TPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNERLCV 127

Qy    274 --PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEA------ALCWRAPGGDP--- 322
Db    128 KFQFLSMLQHHRKRWR------FSFSHFVVD-----PGQEYEVTVHHLPKPIPDGDPNHK 176

Qy    323 --------CQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
Db    177 SKIIFVPDCEDSKMKMTTSCVSSGSLWD-------PNITVETLDTQHLRVDFTLWNEST- 228

Qy    375 PLKDDVLLLETRGPQDNRSLCALEPSGCTSL------PSKASTRAARLGEYLLQDLQSGQ 428
Db    229 PYQ---VLLESFSDSENHS--------CFDVVKQIFAPRQEEFHQRANVTFTLSKFH--- 274

Qy    429 CLQLWDDDLGALWAC-----------------------------------PMDKYIHKR 452
Db    275 -----------WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321

Qy    453 WA---LVWLACLLFAAALSLILLLK----------------------KDHAKAAARGRA 486
Db    322 WVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPRK 381

Qy    487 ALLLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQE 545
Db    382 VWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVES 441

Qy    546 GGVVVLLFSPG--------------AVAL-CSEWLQDGVSGPGAHGPHDAFRASLSCVLP 590
Db    442 NSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPAG----------DLFTAAMNMILP 491

Qy    591 DFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQ 650
Db    492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEMFEPGRMH 551

Qy    651 ERAEQVSRALQPALDSYFHPP 671
Db    552 HVRELTG-------DNYLQSP 565
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RESULT 14
US-09-022-253-2
; Sequence 2, Application US/09022253
; Patent No. 6096305
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6096305el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
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;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,253
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/620,694
;      FILING DATE:  21-MARCH-1996
;      APPLICATION NUMBER:  USSN 08/538,765
;      FILING DATE:  7 AUGUST 1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-253-2

  Query Match             4.4%;  Score 165;  DB 3;  Length 864;
  Best Local Similarity   19.8%;  Pred. No. 7.7e-07;
  Matches  123;  Conservative   79;  Mismatches  209;  Indels  210;  Gaps   31;

Qy    192 PALPW----LNVSADGDNVHLVLN----VSEEQHFGLSLYWNQVQGPP--KPRW--HKNL 239
          |||.|    |||.|.|     :|:    |  ::  |||    :|:        |   |||
Db     14 PALGWLLLLLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDDSWIHPKNL 68

Qy    240 T--GPQIITLN-------HTDLVPCLCIQVWPLEPDS-------------VRTN--IC- 273
          |   |: | :|       | :||| | :: | |: |:             : ||  :|
Db     69 TPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNERLCV 127

Qy    274 --PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEA------ALCWRAPGGDP--- 322
             |    : |:  |:       :   :::|     | :        |   | |||
Db    128 KFQFLSMLQHHRKRWR------FSFSHFVVD-----PGQEYEVTVHHLPKPIPDGDPNHK 176

Qy    323 --------CQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
                  |:    ::   |:   : :       ||: |:   :: |::   || :|
Db    177 SKIIFVPDCEDSKMKMTTSCVSSGSLWD-------PNITVETLDTQHLRVDFTLWNEST- 228

Qy    375 PLKDDVLLLETRGPQDNRSLCALEPSGCTSL------PSKASTRAARLGEYLLQDLQSGQ 428
          | :   :|||:    :| |       |  :      | :          : |
Db    229 PYQ---VLLESFSDSENHS--------CFDVVKQIFAPRQEEFHQRANVTFTLSKFH--- 274

Qy    429 CLQLWDDDLGALWAC-----------------------------------PMDKYIHKR 452
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Db    275 -----------WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321

Qy    453 WA---LVWLACLLFAAALSLILLLK----------------------KDHAKAAARGRA 486
          |    :  :| ||  : : ||: :                       |      | |
Db    322 WVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPRK 381

Qy    487 ALLLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQE 545
            ::|||:   :  :|   |  |       ||:||   : :|  | : |   |::: ::
Db    382 VWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVES 441

Qy    546 GGVVVLLFSPG-------------AVAL-CSEWLQDGVSGPGAHGPHDAFRASLSCVLP 590
            :::| | |              || | |  |    |          | | |::: :||
Db    442 NSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPAG----------DLFTAAMNMILP 491

Qy    591 DFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQ 650
          || :    |:||   |  :     || ||     : |  :  :    :|       ||:

Db    492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEMFEPGRMH 551

Qy    651 ERAEQVSRALQPALDSYFHPP 671
            |          |:|   |
Db    552 HVRELTG-------DNYLQSP 565


RESULT 15
US-09-022-260-2
; Sequence 2, Application US/09022260
; Patent No. 6100235
;  GENERAL INFORMATION:
;    APPLICANT:  Yao, Zhengbin
;    APPLICANT:  Spriggs, Melanie
;    APPLICANT:  Fanslow, William
;    TITLE OF INVENTION:  No. 6100235el Receptor That Binds IL-17
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.5.5
;      SOFTWARE:  Microsoft Word for Apple, Version 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/022,260
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/620,694
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/410,535
;      FILING DATE:  23 MARCH 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2617-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)587-0430
;      TELEFAX:  (206)
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 864 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-022-260-2

  Query Match             4.4%;  Score 165;  DB 3;  Length 864;
  Best Local Similarity   19.8%;  Pred. No. 7.7e-07;
  Matches  123;  Conservative   79;  Mismatches  209;  Indels  210;  Gaps   31;

Qy    192 PALPW----LNVSADGDNVHLVLN----VSEEQHFGLSLYWNQVQGPP--KPRW--HKNL 239
          |||.|    |||.|.|     :|:    |  ::  |||    :|:        |   |||
Db     14 PALGWLLLLLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDDSWIHPKNL 68

Qy    240 T--GPQIITLN-------HTDLVPCLCIQVWPLEPDS-------------VRTN--IC- 273
          |   |: | :|       | :||| | :: | |: |:             : ||  :|
Db     69 TPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNERLCV 127

Qy    274 --PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEA------ALCWRAPGGDP--- 322
             |    : |:  |:       :   :::|     | :        |   | |||
Db    128 KFQFLSMLQHHRKRWR------FSFSHFVVD-----PGQEYEVTVHHLPKPIPDGDPNHK 176

Qy    323 --------CQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
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Db    177 SKIIFVPDCEDSKMKMTTSCVSSGSLWD-------PNITVETLDTQHLRVDFTLWNEST- 228

Qy    375 PLKDDVLLLETRGPQDNRSLCALEPSGCTSL------PSKASTRAARLGEYLLQDLQSGQ 428

Db    229 PYQ---VLLESFSDSENHS--------CFDVVKQIFAPRQEEFHQRANVTFTLSKFH--- 274

Qy    429 CLQLWDDDLGALWAC-----------------------------------PMDKYIHKR 452

Db    275 ------------WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321

Qy    453 WA---LVWLACLLFAAALSLILLLK----------------------KDHAKAAARGRA 486

Db    322 WVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPRK 381

Qy    487 ALLLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQE 545

Db    382 VWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVES 441

Qy    546 GGVVVLLFSPG--------------AVAL-CSEWLQDGVSGPGAHGPHDAFRASLSCVLP 590

Db    442 NSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPAG----------DLFTAAMNMILP 491

Qy    591 DFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQ 650

Db    492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEMFEPGRMH 551

Qy    651 ERAEQVSRALQPALDSYFHPP 671

Db    552 HVRELTG-------DNYLQSP 565
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Search completed: February 24, 2003, 09:23:54
Job time : 24 secs

GenCore version 5.1.3


OM protein - protein search, using sw model

Run on: February 24, 2003, 09:22:01 ; Search time 14 Seconds
(without alignments)
1535.737 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLSLALGRSPVVLS.....TPAPGRGVGPGAGPGAGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters: 156504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3716 | 100.0 | 692 | 10 | US-09-899-471-8 – 2003 | Sequence 8, Appli |
| 2 | 3699.5 | 99.6 | 705 | 9 | US-09-874-503-14 – Geth | Sequence 14, Appl |
| 3 | 3699.5 | 99.6 | 705 | 9 | US-10-000-157-14 | Sequence 14, Appl |
| 4 | 3699.5 | 99.6 | 705 | 9 | US-10-063-547-162 | Sequence 162, App |
| 5 | 3699.5 | 99.6 | 705 | 9 | US-09-816-744-14 | Sequence 14, Appl |
| 6 | 3699.5 | 99.6 | 705 | 9 | US-09-747-259-14 | Sequence 14, Appl |
| 7 | 3699.5 | 99.6 | 705 | 9 | US-10-174-590-598 | Sequence 598, App |
| 8 | 3699.5 | 99.6 | 705 | 9 | US-10-176-758-598 | Sequence 598, App |
| 9 | 3699.5 | 99.6 | 705 | 9 | US-10-063-616-162 | Sequence 162, App |
| 10 | 3699.5 | 99.6 | 705 | 9 | US-10-175-737-598 | Sequence 598, App |
| 11 | 3699.5 | 99.6 | 705 | 9 | US-10-063-502-162 | Sequence 162, App |
| 12 | 3699.5 | 99.6 | 705 | 9 | US-10-173-706-598 | Sequence 598, App |
| 13 | 3699.5 | 99.6 | 705 | 9 | US-10-175-738-598 | Sequence 598, App |
| 14 | 3699.5 | 99.6 | 705 | 9 | US-10-175-752-598 | Sequence 598, App |
| 15 | 3699.5 | 99.6 | 705 | 9 | US-10-176-482-598 | Sequence 598, App |
| 16 | 3699.5 | 99.6 | 705 | 9 | US-10-176-757-598 | Sequence 598, App |
| 17 | 3699.5 | 99.6 | 705 | 9 | US-10-176-913-598 | Sequence 598, App |
| 18 | 3699.5 | 99.6 | 705 | 9 | US-10-180-552-598 | Sequence 598, App |
| 19 | 3699.5 | 99.6 | 705 | 9 | US-10-180-557-598 | Sequence 598, App |
| 20 | 3699.5 | 99.6 | 705 | 9 | US-10-173-700-598 | Sequence 598, App |
| 21 | 3699.5 | 99.6 | 705 | 9 | US-10-174-572-598 | Sequence 598, App |
| 22 | 3699.5 | 99.6 | 705 | 9 | US-10-174-579-598 | Sequence 598, App |
| 23 | 3699.5 | 99.6 | 705 | 9 | US-10-174-582-598 | Sequence 598, App |
| 24 | 3699.5 | 99.6 | 705 | 9 | US-10-174-588-598 | Sequence 598, App |
| 25 | 3699.5 | 99.6 | 705 | 9 | US-10-175-739-598 | Sequence 598, App |
| 26 | 3699.5 | 99.6 | 705 | 9 | US-10-175-740-598 | Sequence 598, App |
| 27 | 3699.5 | 99.6 | 705 | 9 | US-10-175-743-598 | Sequence 598, App |
| 28 | 3699.5 | 99.6 | 705 | 9 | US-10-176-488-598 | Sequence 598, App |
| 29 | 3699.5 | 99.6 | 705 | 9 | US-10-176-492-598 | Sequence 598, App |
| 30 | 3699.5 | 99.6 | 705 | 9 | US-10-176-747-598 | Sequence 598, App |
| 31 | 3699.5 | 99.6 | 705 | 9 | US-10-176-750-598 | Sequence 598, App |
| 32 | 3699.5 | 99.6 | 705 | 9 | US-10-176-985-598 | Sequence 598, App |
| 33 | 3699.5 | 99.6 | 705 | 9 | US-10-176-987-598 | Sequence 598, App |
| 34 | 3699.5 | 99.6 | 705 | 9 | US-10-176-991-598 | Sequence 598, App |
| 35 | 3699.5 | 99.6 | 705 | 9 | US-10-176-992-598 | Sequence 598, App |
| 36 | 3699.5 | 99.6 | 705 | 9 | US-10-176-993-598 | Sequence 598, App |
| 37 | 3699.5 | 99.6 | 705 | 9 | US-10-184-658-598 | Sequence 598, App |
| 38 | 3699.5 | 99.6 | 705 | 9 | US-10-173-695-598 | Sequence 598, App |
| 39 | 3699.5 | 99.6 | 705 | 9 | US-10-173-697-598 | Sequence 598, App |
| 40 | 3699.5 | 99.6 | 705 | 9 | US-10-173-705-598 | Sequence 598, App |
| 41 | 3699.5 | 99.6 | 705 | 9 | US-10-174-576-598 | Sequence 598, App |
| 42 | 3699.5 | 99.6 | 705 | 9 | US-10-174-585-598 | Sequence 598, App |
| 43 | 3699.5 | 99.6 | 705 | 9 | US-10-174-586-598 | Sequence 598, App |
| 44 | 3699.5 | 99.6 | 705 | 9 | US-10-175-747-598 | Sequence 598, App |
| 45 | 3699.5 | 99.6 | 705 | 9 | US-10-176-481-598 | Sequence 598, App |

ALIGNMENTS

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RESULT 1
US-09-899-471-8
; Sequence 8, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
;  APPLICANT: Gao, Zeren
;  TITLE OF INVENTION: Murine Cytokine Receptor
;  FILE REFERENCE: 00-46
;  CURRENT APPLICATION NUMBER: US/09/899,471
;  CURRENT FILING DATE:  2001-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 692
;   TYPE: PRT
;   ORGANISM: Human
US-09-899-471-8

  Query Match           100.0%;  Score 3716;  DB 10;  Length 692;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-296;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
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Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
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Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
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Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
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Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
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Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
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Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480

Qy     481 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR 540

Qy     541 QTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGS 600
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Db     541 QTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGS 600

Qy     601 YVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAL 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 YVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAL 660

Qy     661 QPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
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Db     661 QPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692


RESULT 2
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; Sequence 14, Application US/09874503
; Patent No. US20020177188A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth J.
;  APPLICANT:  Hymowitz,Sarah G.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Starovasnik,Melissa A.
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P3(US)
;  CURRENT APPLICATION NUMBER: US/09/874,503
;  CURRENT FILING DATE:  2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/253,646
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/244,072
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: US 60/242,837
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/175,481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: US 60/191,007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/213,807
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: US 60/172,096
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/138,387
;  PRIOR FILING DATE: 1999-06-09
;  PRIOR APPLICATION NUMBER: US 60/134,287
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/131,022
;  PRIOR FILING DATE: 1999-04-26
;  PRIOR APPLICATION NUMBER: US 60/130,232
;  PRIOR FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: US 60/113,621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: US 60/085,579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 09/854,208
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: US 09/854,280
;  PRIOR FILING DATE: 2001-05-20
;  PRIOR APPLICATION NUMBER: US 09/816,744
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: US 09/747,259
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: US 09/644,848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/380,142
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: US 09/380,138
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: US PCT/US00/34956
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: US PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: US PCT/US00/30873
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: US PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: US PCT/US00/07532
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US PCT/US00/05601
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: US PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: US PCT/US99/31274
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: US PCT/US99/10733
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US PCT/US99/05028
;  PRIOR FILING DATE: 1999-03-08
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-874-503-14

  Query Match             99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
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Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
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Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
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Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
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Qy    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
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Db    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
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Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
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Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
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Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
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Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
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Db    481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy    528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
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RESULT 3
US-10-000-157-14
; Sequence 14, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul L.
;  APPLICANT:  Grimaldi, J.Christopher
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Li, Hanzhong
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Hymowitz, Sarah
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Starovasnik, Melissa.
;  APPLICANT:  VanLookeren, Menno
;  APPLICANT:  Vandlen, Richard
;  APPLICANT:  Watanabe, Colin
;  APPLICANT:  Williams, P.Mickey
;  APPLICANT:  Wood, William
;  APPLICANT:  Yansura, Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P4(US)
;  CURRENT APPLICATION NUMBER: US/10/000,157
;  CURRENT FILING DATE:  2001-10-30
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/130232
;  PRIOR FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: 60/131022
;  PRIOR FILING DATE: 1999-04-26
;  PRIOR APPLICATION NUMBER: 60/134287
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: 60/138387
;  PRIOR FILING DATE: 1999-06-09
;  PRIOR APPLICATION NUMBER: 60/172096
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/175481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: 60/191007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/213807
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/242837
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;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/854280
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/874503
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: 09/908827
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 09/929404
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: 09/931836
;  PRIOR FILING DATE: 2001-08-16
;  PRIOR APPLICATION NUMBER: PCT/US99/05028
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;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05601
;  PRIOR FILING DATE: 2001-03-01
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/07532
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;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
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; PRIOR FILING DATE: 2001-06-20
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-000-157-14

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

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Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
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Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           ||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
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RESULT 4
US-10-063-547-162
; Sequence 162, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-547-162

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

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Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           ||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
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RESULT 5

```
US-09-816-744-14
; Sequence 14, Application US/09816744
; Publication No. US20030003546A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P2(US)
;  CURRENT APPLICATION NUMBER: US/09/816,744
;  CURRENT FILING DATE:  2001-03-22
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-816-744-14

  Query Match            99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity  98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 6
US-09-747-259-14
; Sequence 14, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P1(US)
;  CURRENT APPLICATION NUMBER: US/09/747,259
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/172,096
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: PCT/US99/31274
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: US 60/175,481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/191,007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/07532
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: US 60/213,087
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: US 09/644,848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/242,837
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: PCT/US00/30873
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: US 60/253,646
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
;   LENGTH: 705
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;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-747-259-14

  Query Match             99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 7
US-10-174-590-598
; Sequence 598, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C42
;  CURRENT APPLICATION NUMBER: US/10/174,590
;  CURRENT FILING DATE:  2002-06-18
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-174-590-598

  Query Match             99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 8
US-10-176-758-598
; Sequence 598, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
```

```
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C104
;  CURRENT APPLICATION NUMBER: US/10/176,758
;  CURRENT FILING DATE:  2002-06-21
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-758-598

  Query Match             99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
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RESULT 9
US-10-063-616-162
; Sequence 162, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,616
;  CURRENT FILING DATE:  2002-05-03
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-616-162

  Query Match             99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600
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Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 10
US-10-175-737-598
; Sequence 598, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C50
;  CURRENT APPLICATION NUMBER: US/10/175,737
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-175-737-598

  Query Match            99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity  98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy    528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 11
US-10-063-502-162
; Sequence 162, Application US/10063502
; Publication No. US20030023042A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,502
;  CURRENT FILING DATE:  2002-05-01
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-502-162

  Query Match            99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity  98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
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Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy    528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
```

RESULT 12
US-10-173-706-598
; Sequence 598, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-598

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

```
Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy    528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy    588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy    648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
          |||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
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RESULT 13
US-10-175-738-598
; Sequence 598, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-598

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

```
Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 14
US-10-175-752-598
; Sequence 598, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C60
;  CURRENT APPLICATION NUMBER: US/10/175,752
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-175-752-598

  Query Match             99.6%;  Score 3699.5;  DB 9;  Length 705;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-295;
  Matches  692;  Conservative    0;  Mismatches    0;  Indels   13;  Gaps    1;

Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ------------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705


RESULT 15
US-10-176-482-598
; Sequence 598, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C70
;  CURRENT APPLICATION NUMBER: US/10/176,482
;  CURRENT FILING DATE:  2002-06-20
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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-598

Query Match 99.6%; Score 3699.5; DB 9; Length 705;
Best Local Similarity 98.2%; Pred. No. 3.9e-295;
Matches 692; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

```
Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAK- 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy     480 ----------AAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 527
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS 540

Qy     528 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC 600

Qy     588 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 647
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 VLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSG 660

Qy     648 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 692
           |||||||||||||||||||||||||||||||||||||||||||||
Db     661 RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT 705
```

Search completed: February 24, 2003, 09:25:00
Job time : 16 secs

GenCore version 5.1.3


OM protein - protein search, using sw model

Run on: February 24, 2003, 09:20:41 ; Search time 47 Seconds
(without alignments)
1415.426 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLLSLALGRSPVVLS.....TPAPGRGVGPGAGPGAGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 137.5 | 3.7 | 3707 | 2 | S18252 | heparan sulfate pr |
| 2 | 130.5 | 3.5 | 1366 | 2 | T35985 | probable large Pro |
| 3 | 115.5 | 3.1 | 745 | 2 | H85840 | hypothetical prote |
| 4 | 114.5 | 3.1 | 745 | 2 | C99995 | hypothetical prote |
| 5 | 114.5 | 3.1 | 1193 | 2 | F83264 | hypothetical prote |
| 6 | 113.5 | 3.1 | 761 | 2 | S20458 | pqqF protein - Kle |
| 7 | 111.5 | 3.0 | 478 | 2 | D75564 | hypothetical prote |
| 8 | 108 | 2.9 | 2629 | 2 | T30987 | telomerase-associa |
| 9 | 107 | 2.9 | 719 | 2 | T35189 | probable ATP-depen |
| 10 | 107 | 2.9 | 825 | 1 | A60386 | interleukin-4 rece |
| 11 | 107 | 2.9 | 1118 | 1 | A49724 | protein-tyrosine-p |
| 12 | 104.5 | 2.8 | 238 | 2 | C70841 | hypothetical prote |
| 13 | 104.5 | 2.8 | 975 | 2 | S33121 | homeotic protein C |
| 14 | 104.5 | 2.8 | 1711 | 1 | A55148 | protein-tyrosine-p |
| 15 | 104 | 2.8 | 1487 | 2 | T02850 | hypothetical prote |
| 16 | 103.5 | 2.8 | 676 | 1 | WMBEX6 | UL6 protein - huma |
| 17 | 103.5 | 2.8 | 828 | 2 | AD0412 | ATP-dependent heli |
| 18 | 103.5 | 2.8 | 2055 | 2 | T00093 | hypothetical prote |
| 19 | 103 | 2.8 | 4845 | 2 | T31067 | BIR repeat contain |
| 20 | 101.5 | 2.7 | 1151 | 2 | S48431 | probable membrane |
| 21 | 101 | 2.7 | 274 | 2 | A83583 | probable biotin sy |
| 22 | 100.5 | 2.7 | 709 | 2 | F75584 | hypothetical prote |
| 23 | 100.5 | 2.7 | 741 | 2 | T31164 | hypothetical prote |
| 24 | 100.5 | 2.7 | 753 | 1 | WZBEE8 | gene 56 protein - |
| 25 | 99 | 2.7 | 429 | 2 | T36088 | probable secreted |
| 26 | 99 | 2.7 | 636 | 2 | B83513 | probable heat shoc |
| 27 | 99 | 2.7 | 660 | 2 | E98169 | serine proteinase |
| 28 | 99 | 2.7 | 660 | 2 | AB3118 | serine proteinase |
| 29 | 99 | 2.7 | 679 | 2 | B75262 | conserved hypothet |
| 30 | 98.5 | 2.7 | 724 | 2 | T47149 | hypothetical prote |
| 31 | 98.5 | 2.7 | 741 | 2 | B49555 | enhancer of split |
| 32 | 98.5 | 2.7 | 1737 | 2 | T00209 | MEGF8 protein - hu |
| 33 | 98 | 2.6 | 427 | 2 | E87669 | conserved hypothet |
| 34 | 98 | 2.6 | 1487 | 1 | EDBEE1 | immediate-early pr |
| 35 | 98 | 2.6 | 1487 | 1 | EDBEF6 | 155K transcription |
| 36 | 98 | 2.6 | 2205 | 1 | MNWVRN | nonstructural poly |
| 37 | 97.5 | 2.6 | 418 | 2 | JC7588 | exo-alpha-sialidas |
| 38 | 97.5 | 2.6 | 617 | 2 | F75484 | hypothetical prote |
| 39 | 97.5 | 2.6 | 698 | 2 | A82593 | hypothetical prote |
| 40 | 97.5 | 2.6 | 850 | 2 | JC5700 | ErbB kinase activa |
| 41 | 97.5 | 2.6 | 3739 | 2 | T17410 | polyketide synthas |
| 42 | 97.5 | 2.6 | 4391 | 2 | A38096 | perlecan precursor |
| 43 | 97 | 2.6 | 415 | 2 | T46462 | hypothetical prote |
| 44 | 97 | 2.6 | 779 | 2 | AG1978 | hypothetical prote |
| 45 | 97 | 2.6 | 2594 | 2 | A35774 | kinase-related pro |

ALIGNMENTS

RESULT 1
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.;
J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate prote
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NOO>
A;Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; H
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement mem
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
A;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a g
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G r
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 3.7%; Score 137.5; DB 2; Length 3707;
Best Local Similarity 19.5%; Pred. No. 0.13;

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  Matches  163;  Conservative   73;  Mismatches  235;  Indels  365;  Gaps   42;

Qy       4 PWFLLSLALGRSPVVLSLERLVGPQDAT----HCSP----------------GLSC---- 39
Db     272 PQFLLPSVPGPS--------ACGPQEASCHSGHCIPRDYLCDGQEDCRDGSDELGCASPP 323

Qy      40 ----------------RLWDSDILCLPGDI------------VPAPGPVLAPTHLQTELV 71
Db     324 PCEPNEFACENGHCALKLWRCD-----GDFDCEDRTDEANCSVKQPGEVCGPTHFQCVST 378

Qy      72 LR-------CQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNASLQAQ 124
Db     379 NRCIPASFHCDEESDC-----------------PDRSDEFGCMPPQVVTPPQQ-SIQA- 418

Qy     125 VVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKE 184
Db     419 -------------------------SRGQ---TVTFTCVATGVPTPIINW---------R 441

Qy     185 LNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFG--------------------LSLYW 224
Db     442 LN-WGHIPAHPRVTMTSEGGRGTLIIRDVKEADQGAYTCEAMNSRGMVFGIPDGVLELV- 499

Qy     225 NQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICP----FREDPR 280
Db     500 --PQRGPCPDGHFYLE---DSASCLPCFCFGV---------TNVCQSSLRFRDQIR 541

Qy     281 A---HQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTV 337
Db     542 LSFDQPNDFKGVNVTM---------------------------PSQPGVPPLSSTQLQI 573

Qy     338 DKVL-EFPLLKGHPNLCVQVNSSEKLQLQECLWA----------DSLG------------ 374
Db     574 DPALQEFQL----------VDLSRRFLVHDAFWALPKQFLGNKVDSYGGFLRYKVRYELA 623

Qy     375 -----PL-KDDVLL------LETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQ 422
Db     624 RGMLEPVQKPDVILVGAGYRLHSRGHTPTH------------PGTLNQRQVQLSE---- 666

Qy     423 DLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFA-AALSLILLLKKDHAKAA 481
Db     667 ----------------------EHWVHESGRPVQRAEMLQALASLEAVLLQTVYNTKMA 703

Qy     482 ARGRAALLLYSADDSGFERLVGALASAL--CQLPLRVAVDLWSRRELSAQGPVAWFHAQR 539
Db     704 SVGLSDIVM---DTTVTHTTIHGRAHSVEECRCPIGYS-------GLSCESCDAHF---- 749

Qy     540 RQTLQEGGVVVLLFS----PGAVALC------------SEWLQDGVSGPGAHGPHDAFR 582
Db     750 --TRVPGGPYLGTCSGCNCNGHASSCDPVYGHCLNCQHNTEGPQCDKCKPGFFG--DATK 805

Qy     583 ASLSCVLPDFLQGRAPGSYVGA-------CFDRLLHPDAVPALFRTVPVFT---LPSQLP 632
Db     806 ATATACRP------CPCPYIDASRRFSDTCF---LDTDGQATCDACAPGYTGRRCESCAP 856

Qy     633 DFLGALQQP------------RAPRSGRLQERAEQ-------VSRALQPALDSYFH 669
Db     857 GYEGNPIQPGGKCRPTTQEIVRCDERGSLGTSGETCRCKNNVVGRLCNECSDGSFH 912


RESULT 2
T35985
probable large Pro/Ala/Gly-rich protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T35985
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1999
A;Reference number: Z21589
A;Accession: T35985
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1366 <MUR>
A;Cross-references: EMBL:AL035559; PIDN:CAB37473.1; GSPDB:GN00070; SCOEDB:SC9F2.06c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC9F2.06c

  Query Match             3.5%;  Score 130.5;  DB 2;  Length 1366;
  Best Local Similarity   22.4%;  Pred. No. 0.13;
  Matches  175;  Conservative   57;  Mismatches  238;  Indels  311;  Gaps   42;

Qy      21 LERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDC 80
Db     675 LDGALADPDAGH---PLTIRLLSEVRAALPGP--PAPVPVTRDAVFTAYLDL-------- 721

Qy      81 DLCLRVAVHLAVHGHWEEPEDEEKFGGAA--------DSGVEEPRNASL-QAQVVLSFQA 131
Db     722 -MCLRVATRLA---------DENGLRGTAVRRLAAKVSGQVHEAARRSLGPGQGGLDRES 771

Qy     132 YPT-----------------ARCVLLE-VQVPAAL-----------------VQFGQSVG 156
Db     772 FETLFPCGPAPARLGGGTGWAPAVLAEGLFVPTGSGYRFAHEELADWIQGTHLDLGEALR 831

Qy     157 SVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQ 216
Db     832 ALVHR-RDTPLGT-----------------HTRTLP-VPHHRI---GSVVEALLLLA-RQ 868

Qy     217 HFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFR 276
Db     869 H-----------GVPQ------------LALTLEELVHAL-------------------D 886

Qy     277 EDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEAAL-------CWRAPGGDPCQPLVPP 329
Db     887 RDPHS----WWAARL----LAEALTRVPDATPYTDVLRLLADGIAERAGDGQPTPQVFGP 938

Qy     330 LSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQ 389
Db     939 AFWTAPRVPAATRLDLLR-------------RLVLAD--------------------GPP 965

Qy     390 DNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQL-WDDDLGALWACPMDKY 448
Db     966 H-------EPG-----PRHLDTAAG----LLVADPRTVQPLLVRWFDDERPLPATP---- 1005

Qy     449 IHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAAL-------------LLYSADD 495
Db    1006 ----------------------------HATVATAAQALLHTHRHRGLDGLTEVLVDSTH 1037

Qy     496 SGFERLVGALA----SALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR---------QT 542
Db    1038 RRADELLAVLAEEEPSALCR-----AVERWARDERPARHRAAVTHGLRTAPHARSGADRT 1092

Qy     543 LQEGGVVVLLFSP-------GAVALCSEWLQDGVSGPGAHGPH-----DAFRA------- 583
Db    1093 LLRHAALVLLAGPSDSPLRGGALALL-------VQDPDCRDRHLPAALDLFAACDPYLPP 1145

Qy     584 -SLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFR----TVPVFTLPSQLPDFLGAL 638
Db    1146 SAVAAALPTH-----PEPVLEAFRARLLGPDAGEALRRLADATTPALT--HRVAALVGRT 1198

Qy     639 QQPRAPRSGRLQERAEQVSRAL--QPALDSYFHPPGT------PAPGRGVGPGAGPGAGD 690
Db    1199 VTERPETAGHL---AAYVDRRLDRDPAPRAVLLPLVTRLLDDGPEPARAA--LAGVLAAD 1253

Qy     691 G 691
Db    1254 G 1254


RESULT 3
H85840
hypothetical protein yehQ [imported] - Escherichia coli (strain O157:H7, substrain ED
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Jun-2002
C;Accession: H85840
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
```

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Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85840
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-745 <STO>
A;Cross-references: GB:AE005174; NID:g12516346; PIDN:AAG57188.1; GSPDB:GN00145; UWGP:Z32
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yehQ
C;Superfamily: Escherichia coli hypothetical 68.5K protein (molR-bglX region)

  Query Match             3.1%;  Score 115.5;  DB 2;  Length 745;
  Best Local Similarity   21.4%;  Pred. No. 0.83;
  Matches  162;  Conservative   70;  Mismatches  234;  Indels  291;  Gaps   43;

Qy      21 LERLVGPQDATH------CSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELVLRC 74
           || |    |||        : |::  |:     | ||:|  |  | ::     :   :|
Db     110 LEELATLPDATRKRAQVLVAKGITIELF-----CAPGEIPSARLP-MSDVRFYSRSSIRF 163

Qy      75 QKETDC---DLCLRVAVHLAVHGHWEEPEDEEKF-----------GGAADSGVEEPRNA 119
             :  ||    ||  |   |||    |    : :|           : |    |  ||
Db     164 AR-CDCIEGTLCEHVV--LAVQAFVEAKTQQAEFTHLIWQMRSEHVTSSDDPFASEEGNA 220

Qy     120 SLQ-------------AQVVLSFQA------YPTARCVLLEVQVPAALVQFGQSVGSVV 159
           |              :| :: ::|          ||      |  :| |   ||
Db     221 CRQYVQQLSQALWLGGISQPLIHYEAAFSRAQQAAERCNWR--WVSESLRQLRASV---- 274

Qy     160 YDCFEAA-----LGSEVRIWSYTQPRYEKELNHTQQL---------PALPWLNVSADG-- 203
           | | |       |  :|  :    |    ||  |::         | :|| |   |
Db     275 -DAFHARASHYHAGECLRQLAALNSR----LNCAQEMARRDSVGEVPPVPWRTVVGSGIA 329

Qy     204 -----DNVHLV-LNV---SEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVP 254
                |:: || | :    : :|:|| :::              | |   :: |
Db     330 GEAKLDHLRLVSLGMRCWQDIEHYGLRIWF-------------TDPDTGSILHLS--- 371

Qy     255 CLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWLL--------DAPCS 306
                          |  ||: |    ||  || : |:  |         |  |
Db     372 --------------------RSWPRSEQENSPAATRRLFSFQAGALAGGQIVSQAAKRS 410

Qy     307 LPAEAALCWRAPGGDPCQPLVP--PLSWENVTVDKVLEFPL----------LKGHPNLC 353
             |  |  |    :   :||  | :|      ::|  ||          |:  |  |
Db     411 ADGELLLATR----NRLSSVVPLSPDAW------RMLSAPLRQPGIVALREYLRQRPPSC 460

Qy     354 V----QVNSSEKLQLQECL---WADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLP 406
           :    ||::   | : ||:   |  |   |  |  ::   | :|| |  |      |||
Db     461 IRPLNQVDNLFILPVAECISLGWDSSRQTL--DAQVISGEG-EDN--LLTL------SLP 509

Qy     407 SKASTRAA--RLGEYLLQDLQSGQCL----------------------QLWDDD----- 436
           : ||   |  |:   |||      ||                       : |  |
Db     510 ASASAPYAVERMAA-LLQQTDDPVCLVSGFVSFVDGQLTLEPQVMMTKTRAWALDAETAP 568

Qy     437 ----LGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKD--HAKAAARGRAALLL 490
               | :    |:    |:          ||      || ||     : : :| |:| ||
Db     569 VVASLPSASVLPVPSTAHQ---------LLMRCQALLIQLLHNGWRYQEQSAIGQAELLA 619

Qy     491 YSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVV 550
               || ||   |                                | | |  | |
Db     620 NDLTAVGFYRLAHVL----------------------------GQFRNTESEARVEA 648

Qy     551 LLFSPGAVALCSEWL----QDGVSGPGAHG---------PHDAFR---ASLSCVLPDFLQ 594
           :      | || :      | |:: ||  |         |   ||     |  :||:
Db     649 M---NNGVLLCEQLFPLLQQQGLNRPGFPGECFICELRLPDHRFRWKHNKLFLLLPE--- 702

Qy     595 GRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQL 631
                       |  | ||:   |  :| |  |
Db     703 --------------EHGPAFPAI---VDCYTSPPTL 721


RESULT 4
C99995
hypothetical protein ECs2931 [imported] - Escherichia coli (strain O157:H7, substrain RI

C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: C99995
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C99995
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-745 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36354.1; PID:g13362400; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2931
C;Superfamily: Escherichia coli hypothetical 68.5K protein (molR-bglX region)

  Query Match             3.1%;  Score 114.5;  DB 2;  Length 745;
  Best Local Similarity   21.6%;  Pred. No. 0.99;
  Matches  163;  Conservative   69;  Mismatches  236;  Indels  287;  Gaps   43;

Qy      21 LERLVGPQDATH------CSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELVLRC 74
           || |    |||        : |::  |:     | ||:|  |  | ::     :   :|
Db     110 LEELATLPDATRKRAQVLVAKGITIELF-----CAPGEIPSARLP-MSDVRFYSRSSIRF 163

Qy      75 QKETDC---DLCLRVAVHLAVHGHWEEPEDEEKF-----------GGAADSGVEEPRNA 119
             :  ||    ||  |   |||    |    : :|           :  |    |  ||
Db     164 AR-CDCIEGTLCEHVV--LAVQAFVEAKTQQAEFTHLIWQMRSEHVTSSDDPFASEEGNA 220

Qy     120 SLQ-------------AQVVLSFQA------YPTARCVLLEVQVPAALVQFGQSVGSVV 159
           |              :| :: ::|          ||      |  :| |   ||
Db     221 CRQYVQQLSQALWLGGISQPLIHYEAAFSRAQQAAERCNWR--WVSESLRQLRASV---- 274

Qy     160 YDCFEAA-----LGSEVRIWSYTQPRYEKELNHTQQL---------PALPWLNVSADG-- 203
           | | |       |  :|  :    |    ||  |::         | :|| |   |
Db     275 -DAFHARASHYHAGECLRQLAALNSR----LNCAQEMARRDSVGEVPPVPWRTVVGSGIA 329

Qy     204 -----DNVHLV-LNV---SEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVP 254
                |:: || | :    : :|:|| :::              | |   :: |
Db     330 GEAKLDHLRLVSLGMRCWQDIEHYGLRIWF-------------TDPDTGSILHLS--- 371

Qy     255 CLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWLL--------DAPCS 306
                          |  ||: |    ||  || : |:  |         |  |
Db     372 --------------------RSWPRSEQENSPAATRRLFSFQAGALAGGQIVSQAAKRS 410

Qy     307 LPAEAALCWRAPGGDPCQPLVP--PLSWENVTVDKVLEFPL----------LKGHPNLC 353
             |  |  |    :   :||  | :|      ::|  ||          |:  |  |
Db     411 ADGELLLATR----NRLSSVVPLSPDAW------RMLSAPLRQPGIVALREYLRQRPPSC 460

Qy     354 V----QVNSSEKLQLQECL---WADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLP 406
           :    ||::   | : ||:   |  |   |  |  ::   | :|| |  |      |||
Db     461 IRPLNQVDNLFILPVAECISLGWDSSRQTL--DAQVISGEG-EDN--LLTL------SLP 509

Qy     407 SKASTRAA--RLGEYLLQDLQSGQCL----------------------QLWDDD----- 436
           : ||   |  |:   |||      ||                       : |  |
Db     510 ASASAPYAVERMAA-LLQQTDDPVCLVSGFVSFVDGQLTLEPQVMMTKTRAWALDAETAP 568

Qy     437 ----LGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKD--HAKAAARGRAALLL 490
               | :    |:    |:          ||      || ||     : : :| |:| ||
Db     569 VVASLPSASVLPVPSTAHQ---------LLMRCQALLIQLLHNGWRYQEQSAIGQAELLA 619

Qy     491 YSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVV 550
               || ||   |                                | | |  | |
Db     620 NDLTAVGFYRLAHVL----------------------------GQFRNTESEARVEA 648

Qy     551 LLFSPGAVALCSEWL----QDGVSGPGAHGPHDAFRASLSCVLPD----------FLQGR 596
           :      | || :      | |:: ||   | : |   |   |||          ||
Db     649 M---NNGVLLCEQLFPLLQQQGLNRPGF--PGECFICELR--LPDHRFRWKHNKLFL--- 698

Qy     597 APGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQL 631
                      ||  :  ||    |  :| |  |
Db     699 -----------LLPEEYGPAFPAIVDCYTSPPTL 721
```

RESULT 5
F83264
hypothetical protein PA3063 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83264
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83264
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1193 <STO>
A;Cross-references: GB:AE004730; GB:AE004091; NID:g9949154; PIDN:AAG06451.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3063

Query Match 3.1%; Score 114.5; DB 2; Length 1193;
Best Local Similarity 21.7%; Pred. No. 1.8;
Matches 154; Conservative 53; Mismatches 240; Indels 263; Gaps 38;

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Qy      81 DLCLRVAVHLAVHGHWE--------EPEDEEKFGGAADSGV---EEPRNASLQAQVV--- 126
           || | :|    |   ||          |||       |  |      ||      |::
Db     293 DLRLNMAAG-RVERAWEVGQELLALRPEDRTLLADLARLGEWTGNGPRALGFWKQLLAGA 351

Qy     127 -----------LSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIW- 174
                     || | :     : |   : |      : : ::||        |   |
Db     352 DDPALREHAWRLSLQMFDFDSAIELLAPIGAQRQMTDEELDALVYSHETRGTPEEGEAWL 411

Qy     175 -SYTQPRYEKE----------LNHTQQLPALP--WLNVSADGDNVHLVLNVSEEQHFGLS 221
            | | || |:          | |||||      |  ::      |  |:| |   :
Db     412 RGYVQ-RYPKQRLAWQRLQQILEHTQQLQEETGVWARMAR-----HFPLSVKERMQWA-E 464

Qy     222 LYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPD----------SV 268
            :||     |:  | | | |     :   :          | || |           :
Db     465 THWNLFD--PRQAW-KVLAGVDTRAIREPEFWRLRAALAWALEQDDDARAAYERMLALDI 521

Qy     269 RTN-------ICPFRED--PRAHQNL---WQAAR-----LRLLTLQSWLLDAPC--SLPA 309
           | |        |  :|:    :| | |   || :|       | |   | | |   || |
Db     522 RLNSRDEDQLIALYRDSNPKQALQVLIGSWQRSRDPRRLASALQLAENLHDWPALKSLLA 581

Qy     310 EAALCWRAPGGDPCQPLVPPLSW---------------ENVTVDKVLEFPLLKGHPNLC 353
           ||      | |          |  |              | :  : :: ||
Db     582 EAEGLPEAQGS--------PYYWVARARLAEQEGHGDVAERLYREALVRFP--------- 624

Qy     354 VQVNSSEKLQLQECLW-------ADSLGP---------LKDDV---------LLLETRGP 388
               | |  :  ||         ||| |          |:|             ||||
Db     625 -----GENLVRERLLWFYIDRGRRDSLAPLLAQWHGLALRDSTLWLPFASASLLLE---- 675

Qy     389 QDNRSLC--------------------ALEPSGCTSLPSKASTRAARLGEYLLQDLQSG 427
           :::::|                     ||: ||        :| ||   ||: |
Db     676 RNDQALAWFRLYLKSNPNDWLVQAAYADALDASG---------YQDKALRLRRLLLRRL--- 725

Qy     428 QCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLIL-----LLKKDHAKAAA 482
                 |  |: | |                   ||  | |:      || :  |: |
Db     726 --------DREAVRATPDS---------------FATYLRLLAVAQGPLLAQGEARRAW 761

Qy     483 RGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQT 542
           |  |:|        ||: :  || |  | ||:   | |             :||   :  :
Db     762 NGEPAML-----QLWFEQFLDQLA-ATNQEPLK---DNW----------LAWARGRGLKI 802

Qy     543 LQEGGVVVLLFSPGAVALCSEWLQDGVSGPG---------AHGPHDAFRASLSCVLPDFL 593
           :   :   | |    ||   |: |   |              ||
Db     803 GRNEEIQAALRSQNRAAL-QRLLERGELDPAQRVEALVRLGHG---------------- 844

Qy     594 QGRAPGSYVGACFD-------RLLHPDAVPALFRTVPVFTLPSQLPDFLG 636
           | | |  :||  |         |   |  | ||     |     || |
```

Db 845 -GEALGEALGALGDGHSRDNREQLRRQAAEILERTPQGLQLGWNKRDFGG 893

RESULT 6
S20458
pqqF protein - Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 24-Sep-1999
C;Accession: S20458
R;Meulenberg, J.J.M.; Sellink, E.; Riegman, N.H.; Postma, P.W.
Mol. Gen. Genet. 232, 284-294, 1992
A;Title: Nucleotide sequence and structure of the Klebsiella pneumoniae pqq operon.
A;Reference number: S20452; MUID:92212293; PMID:1313537
A;Accession: S20458
A;Molecule type: DNA
A;Residues: 1-761 <MEU>
A;Cross-references: EMBL:X58778; NID:g43903; PIDN:CAA41584.1; PID:g43909
C;Genetics:
A;Gene: pqqF
C;Superfamily: pyrroloquinoline quinone synthesis F protein

Query Match 3.1%; Score 113.5; DB 2; Length 761;
Best Local Similarity 23.4%; Pred. No. 1.2;
Matches 117; Conservative 50; Mismatches 165; Indels 167; Gaps 27;

```
Qy     282 HQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGG---DPCQPLVPPLSWENVTVD 338
           |:  : | |::|     | |  | || |   |  |       |  |||
Db     182 HRTHYVARRMQL-----W-LQGPQSLEALGELAARFAAGLAAGEAPPPAPPL-------- 227

Qy     339 KVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALE 398
           :: ||  |:      : |:|      |  ||   |  | |:| ||
Db     228 RLGEFTALQ------LAVSS------QPALWRCPLIALSDNVTLLR-------------- 261

Qy     399 PSGCTSLPSKASTRAARLGEYLLQD----LQSGQCLQLWDDDLGALWACPMDKYIHKRWA 454
                              |:|| :    | :|   :    |:   |       :::
Db     262 ------------------EFLLDEAPGSLMAGLRQRRLAGDVALNW-------LYQDRH 295

Qy     455 LVWLACLLFAA---------------ALSLILLLKKDHAKAAARGRAALL---------- 489
           | ||| |:||:                ||      :: |    :| |   |
Db     296 LGWLA-LVFASDRPEEVDRQITHWLQALQQTTPEQQQHYYQLSRRRFQALSPLDQLRQRA 354

Qy     490 ---LYSADDSGFERLVGAL-----ASALCQ-------------LPLRVAVDLWSRRELS 527
              |  :||     ||       |  ||                |||      | ||  |
Db     355 FGFAPGAPPAGFADFCAALQVAPSVSLACQTVSPGEPVATQGFSLPL----SRWRRRPES 410

Qy     528 AQGPVAWFHAQRRQTL-----QEGGVVVLLFSPG--------AVALCSEWLQDGVS---- 570
              |: |    |      ::   :: | |||             ||    :|::
Db     411 DPALAFAFYPQAAGDLVAKCPEKAAPLLHLPSPGDPPRLLLRPPFYCSPDQAEGLARGEQ 470

Qy     571 ---------GPGAHGPHDAFRAS--LSCVLPDFLQGRAPGSYVGACFDRLLHPDA--VPA 617
                    | ||     |  | |:  ||:   || | : : |    :|  | |    |:
Db     471 LRPLLAALRHAGGHGEWHLFDGSWQLTLQLPE--PGRRPEAILQAILRQLALPVASLTPS 528

Qy     618 LFRTVPVFTLPSQLPDFLGALQQPR---APRSGRLQERAEQVSRALQPALDSYFHPPGTP 674
           ::  :  | :|||: ||     :   |  :|   | |: |:| |   : :  :|| |
Db     529 P-ESIAIRHLMAQLPERLGTSGHQKGWLAALAGGSAEDAQWVARQLS-LITAPVNPP-MP 585

Qy     675 APG---RGVGPGAGPGAGD 690
           ||    |||     || ||
Db     586 APAPCRRGVERLVYPG-GD 603
```

RESULT 7
D75564
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: D75564
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

```
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75564
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-478 <WHI>
A;Cross-references: GB:AE001869; GB:AE000513; NID:g6457721; PIDN:AAF09658.1; PID:g645772
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0061
A;Map position: 1

  Query Match             3.0%;  Score 111.5;  DB 2;  Length 478;
  Best Local Similarity   25.7%;  Pred. No. 0.96;
  Matches  105;  Conservative   39;  Mismatches  145;  Indels  119;  Gaps   20;

Qy     276 REDPRAHQNLWQAARLRLLTLQSWLL--------DAPCSLPAEAALCWRAPGGDPCQPLV 327
Db     110 RADPRERPLLREAAQ----RIRRWLARRLARAPGQLPGTVPAHSVLY----AQEEASALS 161

Qy     328 PPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRG 387
Db     162 APAAGDGLT--------LHLGGPD---RLAHWQGLRLS---WR-SLGPNWQLLVQDETSQ 206

Qy     388 PQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDK 447
Db     207 PVSGGQLALLRP----DLPASERQLFLTVGGQQLQVLFSG-----------------DY 244

Qy     448 YIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRA-ALLLYSADDSGFERLVGALA 506
Db     245 VLLRRRA---------DAAQTRHL------ARLAALGRACALLLLPAEQHGRLRLARTLA 289

Qy     507 SALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAV-------- 558
Db     290 RRLRGDPPR-ADDPASGQVAFAQTPAECLAAARR-SLQRLEPLLGRFSPAQVAHEAQVAQ 347

Qy     559 --------------------ALCSEWLQDGVSGP--GAHGPHDAFRASLSCVL----PDF 592
Db     348 ALLHLPPHYAAQVQQAAEHAASAAEPLREAATDPLVGREAGPPVLPATGHFIVFPLGPDP 407

Qy     593 LQGRAPGSYVGACFDRL--LHPDAVPALFRTVPVFTLPSQLPDFLGAL 638
Db     408 LEVRLPG-------DRLLTLRPD-----YRAELVAVLPGQAAVTVGDL 443


RESULT 8
T30987
telomerase-associated protein 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30987
R;Harrington, L.; McPhail, T.; Mar, V.; Zhou, W.; Oulton, R.; Bass, M.B.; Arruda, I.; Ro
Science 275, 973-977, 1997
A;Title: A mammalian telomerase-associated protein.
A;Reference number: Z20952; MUID:97172559; PMID:9020079
A;Accession: T30987
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2629 <HAR>
A;Cross-references: EMBL:U86137; NID:g1835783; PID:g1835784; PIDN:AAC53043.1

  Query Match             2.9%;  Score 108;  DB 2;  Length 2629;
  Best Local Similarity   20.8%;  Pred. No. 16;
  Matches   95;  Conservative   52;  Mismatches  160;  Indels  150;  Gaps   22;

Qy     263 LEPDSVRTNICPFREDPRAHQNL-------------WQAARLRLLTLQSWLLDAPCSLPA 309
Db    1585 LVPDLLEAHVLYASSKPEANQKLPAADVAVFHTFLRQQASLLTQYPL--LLLQQAASQPE 1642

Qy     310 EAALCWRAPGGDPCQ-PLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSS--------- 359
Db    1643 ESPVC--------CQAPLLTQRWHDQFTLKWINKPQTLKGQQSLSLTMSSSPTAVAFSPN 1694

Qy     360 ----------------------EKLQLQECLWADSLGPLKDDVLLLETRGPQ----DNR 392
                                  ||  :  |    |   | |  | | |        | :
Db    1695 GQRAAVGTASGTIYLLNLKTWQEEKAVVSGCDGISSFAFLSDTALFLTTFDGHLELWDLQ 1754

Qy     393 SLC--------ALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACP 444
Db    1755 HGCWVFQTKAHQYQITGCCLSPDRRLLATVCLGGY----------LKLWDTVRGQL---- 1800

Qy     445 MDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVGA 504
Db    1801 AFQYTHPK-------------SLNCVAFHPEGQVVATGSWAGSITFFQADGLKVTKELGA 1847

Qy     505 LASALCQL----PLRV--------AVDLWSRRE------LSAQ----GPVAWFHA-QRRQ 541
Db    1848 PGPSVCSLAFNKPGKIVAVGRIDGTVELWAWQEGARLAAFPAQCGCVSAVLFLHAGDRFL 1907

Qy     542 TLQEGGVVVLL---------------FSPG-AVALCSE-------WLQDGVS----GPGA 574
Db    1908 TAGEDGKAQLWSGFLGRPRGCLGSLPLSPALSVALNPDGDQVAVGYREDGINIYKISSGS 1967

Qy     575 HGP-HDAFRASLSCVL---PDFL-QGRAPGSYVGACF 606
Db    1968 QGPQHQELNVAVSALVWLSPSVLVSGAEDGSLHGWMF 2004


RESULT 9
T35189
probable ATP-dependent DNA helicase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35189
R;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1998
A;Reference number: Z21571
A;Accession: T35189
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-719 <SEE>
A;Cross-references: EMBL:AL022374; PIDN:CAA18513.1; GSPDB:GN00070; SCOEDB:SC5B8.05
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5B8.05

  Query Match             2.9%;  Score 107;  DB 2;  Length 719;
  Best Local Similarity   21.1%;  Pred. No. 3.6;
  Matches  142;  Conservative   75;  Mismatches  221;  Indels  234;  Gaps   36;

Qy      99 PEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSV 158
Db     106 PEDWEAIYGEVERGETDVLLVSPERLNSVDFR-------------DQVLPRLAATTGLL 151

Qy     159 VYDCFEAALGSEVRIWSYT-QPRYEKELNHTQQLPA-LPWLNVSADGDNVHLVLNVSEEQ 216
Db     152 VVD--EAHCISD---WGHDFRPDYRRLRTMLAELPAGVPVLATTATA-NARVTADVAEQL 205

Qy     217 HFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFR 276
Db     206 GTG-------------------AGDALVLRG------------PLDRESLRLGVLVLP 232

Qy     277 EDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVT 336
Db     233 D--AAHRLAWLGERLGEL----------------------PGSGIIYTLTV------AA 261

Qy     337 VDKVLEFPLLKGHP--NLCVQVNSSEKLQLQECLWADSLGPL------------------ 376
Db     262 AEEIAAFLRQRGYPVASYTGKTENADRLQAEEDLLANRVKALVATSALGMGFDKPDLGFV 321

Qy     377 ----------------------KDDVLLLETR---------------GPQDNRSLCA 396
Db     322 VHVGSPSSPIAYYQQVGRAGRGVDHADVLLLPGREDEAIWAYFASVGFPPEEQVRRTLAV 381

Qy     397 LEPSG-CTSLPS---KASTRAARLGEYLLQDLQSGQCLQL----WDDDLGALWACPMDKY 448
Db     382 LEEAGRPMSLPALEPLVDLRRSRL-ETMLKVLDVDGAVKRVKGGW-AATGQAWAYDAERY 439
```

```
Qy    449 IHKRWALVWLACLLFAAALSL------------ILLLKKDHAKAAARGRAALLLYSADDS 496
Db    440 -------AWVARQRQAEQQAMREYVSTTRCRMEFLQRQLDDEKAAPCGRCDTCAGPWLDP 492

Qy    497 GFERLVGALASALCQLPLRVAVDLWSRR-----------ELSAQGPVAWFHAQRRQTLQE 545
Db    493 AVS--AGALAAATGELD-RPGVEVEPRKMWPTGLAAVGMDLKGRIPAG------RQAL-T 542

Qy    546 GGVVVLLFSPGAVALCSEW---LQDGVSGPGAHG--PHDAFRASLSCVLPDFLQGRAPGS 600
Db    543 GRALGRLSDIG-------WGNRLRPLLSAQAADGPVPDDVLRAVVT-VLADW--ARSPGG 592

Qy    601 YVGACFDRLLHPDAVPALFRTVPVFTLPSQL-PDFLGALQQPRAPRSGRLQERAEQVSRA 659
Db    593 WATG------SPDAVA---RPVGVVAVPSRTRPQLVGSLAEGVA-RVGRL---------- 632

Qy    660 LQPALDSYFHPP 671
Db    633 --PLLGSLAHTP 642
```

RESULT 10
A60386
interleukin-4 receptor precursor - human
N;Alternate names: IL-4 receptor
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A60386; A47603
R;Galizzi, J.P.; Zuber, C.E.; Harada, N.; Gorman, D.M.; Djossou, O.; Kastelein, R.; Banc
Int. Immunol. 2, 669-675, 1990
A;Title: Molecular cloning of a cDNA encoding the human interleukin 4 receptor.
A;Reference number: A60386; MUID:91120547; PMID:2278997
A;Accession: A60386
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-825 <GAL>
R;Idzerda, R.L.; March, C.J.; Mosley, B.; Lyman, S.D.; Vanden Bos, T.; Gimpel, S.D.; Din
J. Exp. Med. 171, 861-873, 1990
A;Title: Human interleukin 4 receptor confers biological responsiveness and defines a nc
A;Reference number: A47603; MUID:90171849; PMID:2307934
A;Accession: A47603
A;Molecule type: mRNA
A;Residues: 1-74,'I',76-825 <IDZ>
A;Cross-references: GB:X52425; NID:g33833; PIDN:CAA36672.1; PID:g33834
C;Genetics:
A;Gene: GDB:IL4R
A;Cross-references: GDB:118823; OMIM:147781
A;Map position: 16p12.1-16p12.1
C;Superfamily: interleukin-4 receptor; cytokine receptor homology
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-825/Product: interleukin-4 receptor #status predicted <MAT>
F;26-232/Domain: extracellular #status predicted <EXT>
F;34-218/Domain: cytokine receptor homology <CRS>
F;233-256/Domain: transmembrane #status predicted <TMM>
F;257-825/Domain: intracellular #status predicted <INT>
F;53,98,128,134,176,209/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match  2.9%;  Score 107;  DB 1;  Length 825;
  Best Local Similarity  19.2%;  Pred. No. 4.3;
  Matches  155;  Conservative  66;  Mismatches  284;  Indels  304;  Gaps  36;

```
Qy     41 LWDSDILCLPGDIVP-------APGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVH 93
Db    103 LWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN 162

Qy     94 GHWEEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLE--VQVPAALVQF 151
Db    163 -IWSENDPAD-----------------------FRIY---NVTYLEPSLRIAASTLKS 193

Qy    152 GQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLN 211
```

```
Db    194 GIS------------YRARVRAWAQCY-----NTTWSEWSPSTKWHNSYREPFEQHLLLG 236

Qy    212 VSEEQHFGLSL--------------YWNQVQGPPKPR-------------WHKNLTGPQI 244
Db    237 VSVSCIVILAVCLLCYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQEP 296

Qy    245 ITLNH-----TDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSW 299
Db    297 AKCPHWKNCLTKLLPCF------LEHNMKRD------EDPH------KAA--KEMPFQGS 336

Qy    300 LLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL----------LKGH 349
Db    337 GKSAWCPVEISKTVLW------------PESISVVRCVELFEAPVECEEEEEVEEEKG- 382

Qy    350 PNLCVQVNSSEK----------LQLQECLWADSLGPLKDDVLLLETRG---PQDNRSLCA 396
Db    383 -SFCASPESSRDDFQEGREGIVARLTESLFLDLLG---------EENGGFCQQDMGESCL 432

Qy    397 LEPSGCTS-------LPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYI 449
Db    433 LPPSGSTSAHMPWDEFPSAGPKEAPPWGK--------EQPLHLEPSPPASPTQSPDN--- 481

Qy    450 HKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVGALASAL 509
Db    482 --------LTC------------------------TETPLVIAGNPAYRSFSNSLSQSP 508

Qy    510 CQLPLRVAVDLWSRRELS------------------AQGPVAWFHAQRRQTLQEGGVVV 550
Db    509 C--PRELGPDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNVLQHGAAAA 566

Qy    551 LLFSP--GAVALCSEWLQDGVS-------GPGAHGPHDAFRASL--SCVLPDFLQ-GRAP 598
Db    567 PVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAGYKAFSSLLASSAVSPEKCGFGASS 626

Qy    599 GSYVGACFDRLL-----HPDAVPALFRTVPVFT--------------LPSQLPDFLGA- 637
Db    627 GEEGYKPFQDLIPGCPGDPAPVP-----VPLFTFGLDREPPRSPQSSHLPSSSPEHLGLE 681

Qy    638 -------LQQPRAPRS-----------------------GRLQERAEQVSRALQPALDS 666
Db    682 PGEKVEDMPKPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGGQTPVMAS 741

Qy    667 ---------YFHPPGTPAPGRGVGPGAGP 686
Db    742 PCCGCCCGDRSSPPTTPLRAPDPSPGGVP 770
```

RESULT 11
A49724
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
N;Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SA
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 16-Jun-2000
C;Accession: A49724
R;Matozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita
J. Biol. Chem. 269, 2075-2081, 1994
A;Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase
A;Reference number: A49724; MUID:94124561; PMID:8294459
A;Accession: A49724
A;Molecule type: mRNA
A;Residues: 1-1118 <MATO>
A;Cross-references: GB:D15049; NID:g475003; PIDN:BAA03645.1; PID:g475004
C;Genetics:
A;Gene: GDB:PTPRH; SAP-1
A;Cross-references: GDB:305504
A;Map position: 19q13.4-19q13.4
A;Note: highly expressed in colon and pancreatic cancer cells but not in the normal c
C;Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III re
C;Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric mon
F;1-27/Domain: signal sequence #status predicted <SIG>
F;27-110/Domain: fibronectin type III repeat homology <3FNA>
F;28-1118/Product: protein-tyrosine-phosphatase, receptor type H #status predicted <M
F;28-761/Domain: extracellular #status predicted <EXT>

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F;116-199/Domain: fibronectin type III repeat homology <3FNB>
F;205-289/Domain: fibronectin type III repeat homology <3FNC>
F;296-379/Domain: fibronectin type III repeat homology <3FND>
F;385-468/Domain: fibronectin type III repeat homology <3FNE>
F;474-558/Domain: fibronectin type III repeat homology <3FNF>
F;564-658/Domain: fibronectin type III repeat homology <3FNG>
F;667-737/Domain: fibronectin type III repeat homology <3FNH>
F;762-778/Domain: transmembrane #status predicted <TMN>
F;779-1118/Domain: intracellular #status predicted <INT>
F;846-1070/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;35,78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,470,490,558,5
F;1022/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1028/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             2.9%;  Score 107;  DB 1;  Length 1118;
  Best Local Similarity   20.1%;  Pred. No. 6.3;
  Matches   88;  Conservative   38;  Mismatches  138;  Indels  174;  Gaps   21;

Qy      56 APGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEK------FGGAA 109
           || ||    |::|      |  :   ||            || |:          |
Db     387 APNPV-RNLHMET------QTNSSIALC-----------WEVPDGPYPQDYTYWVGYTG 427

Qy     110 DSGVEEPRNASLQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGS 169
           | |  | ||             |   |  |   |  |  |       |:     | ||
Db     428 DGGGTETRNT-------------TNTSVTAERLEPGTLYTFS------VWAEKNGARGS 467

Qy     170 EVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQG 229
           :  | |      |    |    | | :                ::| |   ||
Db     468 RQNVSISTVP------NAVTSLSKQDWTNST-----------------IALRWTAPQG 502

Qy     230 PPKPRW-------HKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAH 282
           | :  :        : :| |:  : : ||      | :  ||  |:          .  |
Db     503 PGQSSYSYWVSWVREGMTDPRTQSTSGTD------ITLKELEAGSL-----------YH 544

Qy     283 QNLWQAARLRLLTLQSWLLDAPCSLPAEAA-------------LCWRAPGGDPCQPLVPP 329
           :| | |  :    | |  |  : | |               | |:|||    |  |
Db     545 LTVW-AERNEVRGYNSTLTAA--TAPNEVTDLQNETQTKNSVMLWWKAPGDPHSQLYVYW 601

Qy     330 LSWENVTVDKVLEFPLLKGHP-----------NLCVQVNSS-EKLQLQE-------CLWA 370
           : | :             ||||           |   : | :  |::  |        :||
Db     602 VQWAS------------KGHPRRGQDPQANWVNQTSRTNETWYKVEALEPGTLYNFTVWA 649

Qy     371 DSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCL 430
           :    ::||           :||||      :: |  || |
Db     650 E-----RNDV-------ASSTQSLCASTYPDTVTITSCVSTSAGY--------------- 682

Qy     431 QLWDDDLGALWACPMDKY 448
                :  :|:||   |
Db     683 -----GVNLIWSCPQGGY 695


RESULT 12
C70841
hypothetical protein Rv2102 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70841
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70841
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <COL>
A;Cross-references: GB:AL021924; GB:AL123456; NID:g3261519; PIDN:CAA17285.1; PID:e125238
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2102

  Query Match             2.8%;  Score 104.5;  DB 2;  Length 238;
  Best Local Similarity   25.9%;  Pred. No. 1.4;
  Matches   55;  Conservative   21;  Mismatches   93;  Indels   43;  Gaps   10;

Qy     495 DSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFS 554
           |:|   || ||       | |: :       : | |   | | :|  || |
Db      29 DAG---LVTALVQGSRARPYRIRIG------IPAFGKSQWAHVER--TLAENAWYAAKLL 77

Qy     555 PGAVALCSEWLQDGVSGPG-AHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPD 613
           | :    | ::|  :| | :  |  |   || |  ||:     |  :: | |  |
Db      78 SGEM---PEDIEDVFAGLGLSLFPGTARELSLDCSCPDY---AVPCKHLAATFYLLAES- 130

Qy     614 AVPALFRTVPVFTLP---SQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYF-- 668
               |   |    |       :  | |  |   ||  :    : ||||:: |   || |:
Db     131 -----FDEDPFAILAWRGREREDLLANLAAARADGAAPAADHAEQVAQPLTDCLDRYYAR 185

Qy     669 -------HPPGTPA-------PGRGVGPGAGP 686
                  || ||:       |  |:     |
Db     186 QADINVPSPPATPSTALLDQLPDTGLSARGRP 217


RESULT 13
S33121
homeotic protein CDP - dog (fragment)
N;Alternate names: CCAAT displacement protein; homeotic protein Clox
C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S33121
R;Andres, V.; Nadal-Ginard, B.; Mahdavi, V.
Development 116, 321-334, 1992
A;Title: Clox, a mammalian homeobox gene related to Drosophila cut, encodes DNA-bindi
A;Reference number: S33121; MUID:93161940; PMID:1363085
A;Accession: S33121
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-975 <AND>
A;Cross-references: EMBL:X69017; NID:g2201; PIDN:CAA48782.1; PID:g2202
C;Superfamily: homeotic protein CDP; cut repeat homology; homeobox homology
C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation
F;1-67/Domain: cut repeat homology (fragment) <CU1>
F;383-455/Domain: cut repeat homology <CU2>
F;566-638/Domain: cut repeat homology <CU3>
F;685-741/Domain: homeobox homology <HOX>

  Query Match             2.8%;  Score 104.5;  DB 2;  Length 975;
  Best Local Similarity   20.4%;  Pred. No. 8.3;
  Matches  174;  Conservative   74;  Mismatches  244;  Indels  363;  Gaps   44;

Qy       3 VPWFLLSLALGRSPVVLSLERLVGPQDATHCS-------PGLSCRLWDSDILCLPGDIVP 55
           :|   :|      |: |||::   |  |   |       |  |      |:  | |||
Db     190 IPSSPMSSVSSYPPLALSLKK---PPTAPDTSASTLPNPPALKKESQDAPGLDLPGAAES 246

Qy      56 APGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEE--------------PE 100
           | |            |||            |   |   | |::                ||
Db     247 AQG------------VLR-----------HVKSELGRSGVWKDHWWSTVQPERKSAAPPE 283

Qy     101 D--EEKFGGAADSG-----------------------------------------------V 113
           |   |: ||  : |
Db     284 DAKSEEAGGTKEKGGGQGHGPIAASSRDPHHRRSTGRNGPALSPRTPQSSELSLTGASRS 343

Qy     114 EEPRNASLQAQ--VVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEV 171
           | |:|: | :   | :|  | |                    ||  :  : :|  :  ||
Db     344 ETPQNSPLPSSPIVPMSKPAKP-------------------SVPPLTPEQYEIYMYQEV 383

Qy     172 RIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGP- 230
               |:   ||              :: :|    :   :  |:  |||      ||
Db     384 DTIELTRQVKEK--------------LAKNG----ICQRIFGEKVLGLS------QGSV 418

Qy     231 ------PKPRWHKNLTGPQIITLNHTDLVPCLCIQVW---------------------- 261
                 |||  | |          |      | : :|:|
Db     419 SDMLSRPKP-WSK---------LTQKGREPFIRMQLWLNGELGQGVLPVQGQQQGPVLHS 468

Qy     262 ------PLEPDSVRTNICPFRE---DPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEAA 312
```

```
Db    469 VTSLQDPLQQGCVSSESTPKTSASCSPAPESPMSSSESVKSLT---ELVQQPCP-PIET- 523

Qy    313 LCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL-LKGHPNLCVQ--VNSSEKL------- 362

Db    524 ----SKDGKPPEPSDPPAS------DSQPATPLPLSGHSALSIQELVAMSPELDTYGITK 573

Qy    363 QLQECLWADSLGP-LKDDVLLLETRG----------PQDNRSLCALEPSGCTSLPSKAST 411

Db    574 RVKEVLTDNNLGQRLFGETILGLTQGSVSDLLSRPKPWHKLSLKGREPF----------622

Qy    412 RAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLIL 471

Db    623 ---------------VRMQLWLND-------PNN-------------------VEKLM 639

Qy    472 LLKKDHAKAAARGRAALLLYSADDS--------GFERLVG-------------------- 503

Db    640 DMKRMEKKAYMKRRHS----SVSDSQPCEPPSVGIDYSQGASPQPQHQLKKPRVVLAPEE 695

Qy    504 --ALASALCQLPL---RVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAV 558

Db    696 KEALKRAYQQKPYPSPKTIEELATQLNLKTSTVINWFHNYRSRIRRE------------- 742

Qy    559 ALCSEWLQDGVSG-PGA-HGPHDAFRASLSCVLPDFLQGRAPGSYVGAC--FDRLLHPDA 614

Db    743 -LFIEEIQAGSQGQAGARHSP--SARSS----------GAAPSSEGDSCDGVEAAEGPGA 789

Qy    615 VPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGT- 673

Db    790 ADA-EESAPAAAAKSQ----GGPAEAAVAP-----EEREE----APRPAEKRSRRPRGPG 835

Qy    674 PAPGRGVGPGAGPGA 688

Db    836 PGPGRRGGGGPAPGA 850
```

RESULT 14
A55148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
N;Alternate names: OST-PTP; osteotesticular protein-tyrosine-phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55148
R;Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.
J. Biol. Chem. 269, 30659-30667, 1994
A;Title: Identification of a hormonally regulated protein tyrosine phosphatase associate
A;Reference number: A55148; MUID:95074080; PMID:7527035
A;Accession: A55148
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1711 <MAU>
A;Cross-references: GB:L36884
C;Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosi
C;Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III rep
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MA
F;1174-1398/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1350/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1356/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             2.8%;  Score 104.5;  DB 1;  Length 1711;
  Best Local Similarity   18.8%;  Pred. No. 17;
  Matches  150;  Conservative   80;  Mismatches  274;  Indels  293;  Gaps   37;

```
Qy      5 WFLLSLALG-RSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPVLAP 63

Db    322 WASWKAGLGARDGYVL---KLSGPMESTSTLGPEECN------------AVFPGP-LPP 364

Qy     64 THLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEE----PRNA 119

Db    365 GHYTLQL-------------------------------KVLAGPYDAWVEGSTWLAESA 392

Qy    120 SLQAQVV--------LSFQAYPTARCVLLEVQVPAALVQFGQSVGS--VVYDCFEAALGS 169

Db    393 ALPREVPGARLWLDGLEASKQPGRRALLYSDDAPGSLGNISVPSGATHVIFCGLVPGAHY 452

Qy    170 EVRIWSYTQPRYEKELNHTQQLP--ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQV 227

Db    453 RVDIASSTGDISQSISGYTSPLPPQSLEVISRSSPSD--------------LTIAWGPA 497

Qy    228 QGP---PKPRWHKNLT----------GPQIITLNHTDLVP--CLCIQVWP----LEPDSV 268

Db    498 PGQLEGYKVTWHQDGSQRSPGDLVDLGPDTLSLTLKSLVPGSSYTVSAWAWAGNLGSDSQ 557

Qy    269 RTNICP-----------FREDPRAHQNLW-----------QAARLRLLTLQ-------- 297

Db    558 KIHSCTRPAPPTNLSLGFAHQPAALKASWYHPPGGRDAFHLRLYRLRPLTLESEKVLPRE 617

Qy    298 ----SWL-LDAPCSLPAEAALCW--------RAPGGDPCQPLVPPLSWENVTVDKVLEFP 344

Db    618 AQNFSWAQLTAGCEFQVQLSTLWGSERSSSANATGWTP--PSAPTL--VNVTSDAPTQLQ 673

Qy    345 LLKGHPNLCVQVNSSEKLQLQECLWADS-------LGPLKDDVLLLETRGPQDNRSLCAL 397

Db    674 VSWAHV-------PGGRSRYQVTLYQESTRTATSIMGP------------KEDGTSFLGL 714

Qy    398 EPS-----GCTSLPSKASTRAARLGEY--------LLQDLQSGQCLQLWDDDLGALWACP 444

Db    715 TPGTKYKVEVISWAGPLYTAAANVSAWTYPLIPNELLVSMQAGSAVV------------- 761

Qy    445 MDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVGA 504

Db    762 ---------NLAWPSGPLGQGAC---------HAQLSDAGHLS----------------- 786

Qy    505 LASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEG-GVVVLLFSPGAVALCSE 563

Db    787 -----WEQPLKLGQELFMLRDLTPGHTISMSVRCRAGPLQASTHLVVLSVEPGPV----- 836

Qy    564 WLQDGVSGPGAHGPHDAFRASLSCVLPD--------FLQGRAPGS------YVGACFDRL 609

Db    837 --EDVLCHP------EATYLALNWTMPAGDVDVCLVVVERLVPGGGTHFVFQVNTSGDAL 888

Qy    610 LHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFH 669

Db    889 LLPNLMPTTSYRLSLTVL-----------------GRNSRWSRAVSLVCSTSAEAW-H 928

Qy    670 PPGTPAP-----GRGVG 681

Db    929 PPELAEPPQVELGTGMG 945
```

RESULT 15
T02850
hypothetical protein L1439.2 [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C;Accession: F81462; T02850
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protei
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: F81462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1487 <PYL>
A;Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24673.1; PID:g2266918; GSPDB:G
A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: L1439.2
A;Map position: 1

  Query Match             2.8%;  Score 104;  DB 2;  Length 1487;
  Best Local Similarity   23.7%;  Pred. No. 15;
  Matches   63;  Conservative   19;  Mismatches  112;  Indels   72;  Gaps    9;

```
Qy     444 PMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVG 503
           |:|   |         |   ||| :   ::        |||  | |  | :|:
Db      19 PLDAQGH--------VCHARAAATAPATVVSNAEEVTEARGSCAPLHASREDT--RDRDS 68

Qy     504 ALASALCQLPLRVAVDLWSRR-------ELSAQGPVAWFHAQRRQTL----QEGGVVVLL 552
            :|:   | |   | | |  |'        |:  | |   |   : :    |:||
Db      69 PVAAPQRQQPALNAEDEWRWRASRPASSASSSSSPSAQDEAHSDRVVYEDGQDGG----- 123

Qy     553 FSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHP 612
               |   |||        || |  |   || |                       |||
Db     124 --EEAADRSSEWRHS-----GADGASDDAEASSSTA--------------------LHP 155

Qy     613 DAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPG 672
            : | | :      |||  |      || : |            |    | |:|   ||
Db     156 PSPPQLHQQEASPLLPSLTPVATACTQQAKPP-----------STTAPPGLESDTPPPQ 203

Qy     673 TPAPGRGVGP------GAGPGAGDGT 692
             : |:|  |         | :|  |
Db     204 VVSQGKGTDPAKRLCTAVAPASGRAT 229
```

Search completed: February 24, 2003, 09:23:35
Job time : 58 secs

GenCore version 5.1.3


OM protein - protein search, using sw model

Run on: February 24, 2003, 09:19:21 ; Search time 14 Seconds
(without alignments)
2050.116 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLSLALGRSPVVLS.....TPAPGRGVGPGAGPGAGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 173 | 4.7 | 866 | 1 | I17R_HUMAN | Q96f46 homo sapien |
| 2 | 165 | 4.4 | 864 | 1 | I17R_MOUSE | Q60943 mus musculu |
| 3 | 137.5 | 3.7 | 3707 | 1 | PGBM_MOUSE | Q05793 mus musculu |
| 4 | 118.5 | 3.2 | 1711 | 1 | PTPO_RAT | Q64612 rattus norv |
| 5 | 113.5 | 3.1 | 761 | 1 | PQQF_KLEPN | P27508 klebsiella |
| 6 | 112.5 | 3.0 | 1208 | 1 | RCQ4_HUMAN | O94761 homo sapien |
| 7 | 108.5 | 2.9 | 925 | 1 | W70T_HUMAN | P57737 homo sapien |
| 8 | 107 | 2.9 | 825 | 1 | IL4R_HUMAN | P24394 homo sapien |
| 9 | 107 | 2.9 | 2003 | 1 | NTC4_HUMAN | Q99466 homo sapien |
| 10 | 104.5 | 2.8 | 975 | 1 | CUT1_CANFA | P39881 canis famil |
| 11 | 103.5 | 2.8 | 676 | 1 | UL06_HSV11 | P10190 herpes simp |
| 12 | 102 | 2.7 | 922 | 1 | W70T_MOUSE | Q9d2v7 mus musculu |
| 13 | 101.5 | 2.7 | 1151 | 1 | ATC7_YEAST | P40527 saccharomyc |
| 14 | 100.5 | 2.7 | 753 | 1 | UL06_HSVEB | P28944 equine herp |
| 15 | 100.5 | 2.7 | 3312 | 1 | CLR3_HUMAN | Q9nyq7 homo sapien |
| 16 | 99 | 2.7 | 955 | 1 | CHRD_HUMAN | Q9h2x0 homo sapien |
| 17 | 99 | 2.7 | 1011 | 1 | M3K6_HUMAN | O95382 homo sapien |
| 18 | 98.5 | 2.7 | 546 | 1 | AAAS_MOUSE | P58742 mus musculu |
| 19 | 98.5 | 2.7 | 587 | 1 | NDC2_RAT | P70545 rattus norv |
| 20 | 98.5 | 2.7 | 741 | 1 | TLE4_RAT | Q07141 rattus norv |
| 21 | 98.5 | 2.7 | 766 | 1 | TLE4_HUMAN | Q04727 homo sapien |
| 22 | 98.5 | 2.7 | 766 | 1 | TLE4_MOUSE | Q62441 mus musculu |
| 23 | 98.5 | 2.7 | 948 | 1 | CHRD_MOUSE | Q9z0e2 mus musculu |
| 24 | 98.5 | 2.7 | 1505 | 1 | CUT1_HUMAN | P39880 homo sapien |
| 25 | 98.5 | 2.7 | 1524 | 1 | Y133_HUMAN | Q14146 homo sapien |
| 26 | 98 | 2.6 | 1487 | 1 | ICP4_HSVEB | P28925 equine herp |
| 27 | 98 | 2.6 | 1487 | 1 | ICP4_HSVEK | P17473 equine herp |
| 28 | 98 | 2.6 | 2205 | 1 | POLN_RUBVT | P13889 rubella vir |
| 29 | 97.5 | 2.6 | 418 | 1 | NER3_RAT | Q99pw5 rattus norv |
| 30 | 97.5 | 2.6 | 850 | 1 | NRG2_HUMAN | O14511 homo sapien |
| 31 | 97.5 | 2.6 | 4393 | 1 | PGBM_HUMAN | P98160 homo sapien |
| 32 | 97 | 2.6 | 2594 | 1 | 7LES_DROVI | P20806 drosophila |
| 33 | 96.5 | 2.6 | 392 | 1 | GAG_BLVAU | P25058 bovine leuk |
| 34 | 95.5 | 2.6 | 505 | 1 | CXAA_MOUSE | Q9wus4 mus musculu |
| 35 | 95 | 2.6 | 862 | 1 | CUT1_RAT | P53565 rattus norv |
| 36 | 94.5 | 2.5 | 614 | 1 | YEHQ_ECOLI | P33353 escherichia |
| 37 | 94 | 2.5 | 993 | 1 | AFSR_STRCO | P25941 streptomyce |
| 38 | 94 | 2.5 | 1446 | 1 | IE18_PRVKA | P33479 pseudorabie |
| 39 | 93.5 | 2.5 | 642 | 1 | FZD1_MOUSE | O70421 mus musculu |
| 40 | 93.5 | 2.5 | 713 | 1 | GAC1_HUMAN | O75325 homo sapien |
| 41 | 93.5 | 2.5 | 890 | 1 | TYO3_HUMAN | Q06418 homo sapien |
| 42 | 93 | 2.5 | 672 | 1 | NQO3_PARDE | P29915 paracoccus |
| 43 | 92 | 2.5 | 428 | 1 | NER3_HUMAN | Q9uq49 homo sapien |
| 44 | 92 | 2.5 | 553 | 1 | MIS_RAT | P49000 rattus norv |
| 45 | 92 | 2.5 | 632 | 1 | GIDA_BACHD | Q9rca8 bacillus ha |

ALIGNMENTS

RESULT 1
I17R_HUMAN
ID I17R_HUMAN STANDARD; PRT; 866 AA.
AC Q96F46; O43844;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-17 receptor precursor (IL-17 receptor).
GN IL17R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=98035683; PubMed=9367539;
RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
RA VandenBos T., Zappone J., Painter S.L., Armitage R.J.;
RT "Molecular characterization of the human interleukin (Il)-17
RT receptor.";
RL Cytokine 9:794-800(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
CC suggesting that additional components are involved in IL17-induced
CC signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- PTM: Glycosylated.
CC ---

CC ---
DR EMBL; U58917; AAB99730.1; -.
DR EMBL; BC011624; AAH11624.1; -.
DR Genew; HGNC:5985; IL17R.
DR MIM; 605461; -.
KW Receptor; Transmembrane; Signal; Glycoprotein.

| | | | |
|---|---|---|---|
| FT | SIGNAL | 1 | 31 | POTENTIAL. |
| FT | CHAIN | 32 | 866 | INTERLEUKIN-17 RECEPTOR. |
| FT | DOMAIN | 32 | 320 | EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM | 321 | 341 | POTENTIAL. |
| FT | DOMAIN | 342 | 866 | CYTOPLASMIC (POTENTIAL). |
| FT | DOMAIN | 810 | 818 | POLY-GLU. |
| FT | CARBOHYD | 49 | 49 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 54 | 54 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 206 | 206 | N-LINKED (GLCNAC. . .) (POTENTIAL). |

```
FT   CARBOHYD     225    225       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     242    242       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     265    265       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     367    367       V -> A (IN REF. 1).
FT   CONFLICT     580    580       H -> R (IN REF. 1).
SQ   SEQUENCE   866 AA;  96131 MW;  28330BED2303B0C9 CRC64;

  Query Match             4.7%;  Score 173;  DB 1;  Length 866;
  Best Local Similarity   21.3%;  Pred. No. 7.8e-06;
  Matches  117;  Conservative   76;  Mismatches  191;  Indels  166;  Gaps   31;

Qy    237 KNLT--GPQIITLN----HT---DLVPCLCIQVWPLEPDS-------------VRTN-- 271
          :|||   |: : :     ||   || |   |: | |: |:                 : ||
Db     66 RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIE-WTLQTDASILYLEGAELSVLQLNTNER 124

Qy    272 IC---PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCS-------LPAEAALCWRAPGGD 321
          :|    |    | |   |:       |   :::|           ||         | ||
Db    125 LCVRFEFLSKLRHHHRRWR------FTFSHFVVDPDQEYEVTVHHLPKP------IPDGD 172

Qy    322 PCQP----LVPPLSWENVTVDKVLEFPLLKG----HPNLCVQVNSSEKLQLQECLWADSL 373
          |       |||      : |      | :       ||: |:   : :|::   || :|
Db    173 PNHQSKNFLVPDCEHARMKVTT----PCMSSGSLWDPNITVETLEAHQLRVSFTLWNES- 227

Qy    374 GPLKDDVLLLETRGPQDNRSLCALEPSGCTS----LPSKASTRAARLGEY--------LL 421
              :| |  |         :|   |      :|      | |  |:          |
Db    228 ----THYQILLTSFPH-------MENHSCFEHMHHIP------APRPEEFHQRSNVTLTL 270

Qy    422 QDLQS------------GQCLQLWDDDL--GALWACP-----------MDKYIHKRWAL 455
          ::|:                ||   :| |   |  :||           |  :::  | :
Db    271 RNLKGCCRHQVQIQPFFSSCL---NDCLRHSATVSCPEMPDTPEPIPDYMPLWVY--WFI 325

Qy    456 VWLACLLFAAALSLILLLK----------------------KDHAKAAARGRAALLLYS 492
            :: ||  : : ||: :                       |     : |   ::||
Db    326 TGISILLVGSVILLIVCMTWRLAGPGSEKYSDDTKYTDGLPVADLIPPPLKPRKVWIIYS 385

Qy    493 ADDSGFERLVGALAS-ALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVL 551
          ||   :  :|   |   |     ||:||   : :|  | : |   |::: ::    :::
Db    386 ADHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIV 445

Qy    552 LFSPGAVALCSEWLQDGVSGPGA-------HGP--HDAFRASLSCVLPDFLQGRAPGSYV 602
          | | |  |   :|    : | ||       ||    | | |::: :|||| :    |:||
Db    446 LCSRGTRA---KW--QALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACFGTYV 500

Qy    603 GACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQP 662
            |  :     || ||   | : |  :   :|     : ||:  |  ::|
Db    501 VCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGRM-HRVGELSG---- 555

Qy    663 ALDSYFHPPG 672
            |:|   ||
Db    556 --DNYLRSPG 563


RESULT 2
I17R_MOUSE
ID   I17R_MOUSE     STANDARD;      PRT;   864 AA.
AC   Q60943;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-17 receptor precursor (IL-17 receptor).
GN   IL17R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymic lymphoma;
RX   MEDLINE=96111968; PubMed=8777726;
RA   Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,
RA   Comeau M.R., Cohen J.I., Spriggs M.K.;
RT   "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
RT   novel cytokine receptor.";
RL   Immunity 3:811-821(1995).
CC   -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
CC       suggesting that additional components are involved in IL17-induced
CC       signaling (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U31993; AAC52357.1; -.
DR   MGD; MGI:107399; Il17r.
KW   Receptor; Transmembrane; Signal; Glycoprotein.
FT   SIGNAL       1     31       POTENTIAL.
FT   CHAIN       32    864       INTERLEUKIN-17 RECEPTOR.
FT   DOMAIN      32    322       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   323    343       POTENTIAL.
FT   DOMAIN     344    864       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     809    814       POLY-GLU.
FT   CARBOHYD    54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   206    206       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   225    225       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   242    242       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   265    265       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   864 AA;  97807 MW;  343FD51AA687DA31 CRC64;

  Query Match             4.4%;  Score 165;  DB 1;  Length 864;
  Best Local Similarity   19.8%;  Pred. No. 3.4e-05;
  Matches  123;  Conservative   79;  Mismatches  209;  Indels  210;  Gaps   31;

Qy    192 PALPW----LNVSADGDNVHLVLN----VSEEQHFGLSLYWNQVQGPP--KPRW--HKNL 239
          |||  |    |||  | |      :|:    |  ::  |||    :|:        |   |||
Db     14 PALGWLLLLLNVLAPGRASPRLLDFPAPVCAQE--GLSC---RVKNSTCLDDSWIHPKNL 68

Qy    240 T--GPQIITLN-------HTDLVPCLCIQVWPLEPDS-------------VRTN--IC- 273
          |   |: | :|        | :||| | :: | |: |:                : ||  :|
Db     69 TPSSPKNIYINLSVSSTQHGELVPVLHVE-WTLQTDASILYLEGAELSVLQLNTNERLCV 127

Qy    274 --PFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEA------ALCWRAPGGDP--- 322
              |   : |:  |:        :   :::|     | :        |    | |||
Db    128 KFQFLSMLQHHRKRWR------FSFSHFVVD-----PGQEYEVTVHHLPKPIPDGDPNHK 176

Qy    323 --------CQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
                 |:     ::   |:   : :       ||: |:   :: |::   || :|
Db    177 SKIIFVPDCEDSKMKMTTSCVSSGSLWD-------PNITVETLDTQHLRVDFTLWNEST- 228

Qy    375 PLKDDVLLLETRGPQDNRSLCALEPSGCTSL------PSKASTRAARLGEYLLQDLQSGQ 428
          | :   :|||:    :| |       |  :      | :          : |
Db    229 PYQ---VLLESFSDSENHS--------CFDVVKQIFAPRQEEFHQRANVTFTLSKFH--- 274

Qy    429 CLQLWDDDLGALWAC-----------------------------------PMDKYIHKR 452
                    | |                                     |:  ||
Db    275 -----------WCCHHHVQVQPFFSSCLNDCLRHAVTVPCPVISNTTVPKPVADYI-PL 321

Qy    453 WA---LVWLACLLFAAALSLILLLK----------------------KDHAKAAARGRA 486
          |    :  :| ||  : : ||: :                        |      | |
Db    322 WVYGLITLIAILLVGSVIVLIICMTWRLSGADQEKHGDDSKINGILPVADLTPPPLRPRK 381

Qy    487 ALLLYSADDSGFERLVGALASAL-CQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQE 545
            ::||||    :  :|   |  |       ||:||   : :|  | : |   |::: ::
Db    382 VWIVYSADHPLYVEVVLKFAQFLITACGTEVALDLLEEQVISEVGVMTWVSRQKQEMVES 441

Qy    546 GGVVVLLFSPG-------------AVAL-CSEWLQDGVSGPGAHGPHDAFRASLSCVLP 590
            :::| | |                || | |  |   |           | | |::: :||
Db    442 NSKIIILCSRGTQAKWKAILGWAEPAVQLRCDHWKPAG----------DLFTAAMNMILP 491

Qy    591 DFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQ 650
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          || :    |:||   |  :     || ||     : |  :  :    :|'      ||:
Db    492 DFKRPACFGTYVVCYFSGICSERDVPDLFNITSRYPLMDRFEEVYFRIQDLEMFEPGRMH 551

Qy    651 ERAEQVSRALQPALDSYFHPP 671
              |          |:|   |
Db    552 HVRELTG-------DNYLQSP 565


RESULT 3
PGBM_MOUSE
ID   PGBM_MOUSE     STANDARD;      PRT;  3707 AA.
AC   Q05793;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Basement membrane-specific heparan sulfate proteoglycan core
DE   protein precursor (HSPG) (Perlecan) (PLC).
GN   HSPG2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Melanoma;
RX   MEDLINE=92078153; PubMed=1744087;
RA   Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M.,
RA   Yamada Y., Hassell J.R.;
RT   "The complete sequence of perlecan, a basement membrane heparan
RT   sulfate proteoglycan, reveals extensive similarity with laminin A
RT   chain, low density lipoprotein-receptor, and the neural cell adhesion
RT   molecule.";
RL   J. Biol. Chem. 266:22939-22947(1991).
RN   [2]
RP   SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=89034110; PubMed=2972708;
RA   Noonan D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M.,
RA   Yamada Y., Hassell J.R.;
RT   "Identification of cDNA clones encoding different domains of the
RT   basement membrane heparan sulfate proteoglycan.";
RL   J. Biol. Chem. 263:16379-16387(1988).
CC   -!- FUNCTION: This protein is an integral component of basement
CC       membranes. It is responsible for the fixed negative electrostatic
CC       charge and is involved in the charge-selective ultrafiltration
CC       properties. It serves as an attachment substrate for cells.
CC   -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC       dimers or stellate structures. It interacts with other basement
CC       membrane components such as laminin, prolargin and collagen type
CC       IV.
CC   -!- SUBCELLULAR LOCATION: Extracellular.
CC   -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
CC   -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC       AND O-LINKED OLIGOSACCHARIDES.
CC   -!- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
CC   -!- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
CC   -!- SIMILARITY: CONTAINS 15 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 SEA DOMAIN.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M77174; AAA39911.1; -.
DR   EMBL; J04054; AAA39899.1; -.
DR   EMBL; J04055; AAA39912.1; -.
DR   HSSP; P01130; 1AJJ.
DR   MGD; MGI:96257; Hspg2.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR002172; LDL_recept_A.
DR   InterPro; IPR000034; Laminin_B.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR000082; SEA_domain.
DR   Pfam; PF00008; EGF; 4.
DR   Pfam; PF00047; ig; 15.
DR   Pfam; PF00052; laminin_B; 3.
DR   Pfam; PF00053; laminin_EGF; 8.
DR   Pfam; PF00054; laminin_G; 3.
DR   Pfam; PF00057; ldl_recept_a; 4.
DR   Pfam; PF01390; SEA; 1.
DR   PRINTS; PR00010; EGFBLOOD.
DR   ProDom; PD003031; Laminin_B; 3.
DR   SMART; SM00180; EGF_Lam; 7.
DR   SMART; SM00001; EGF_like; 6.
DR   SMART; SM00408; IGc2; 14.
DR   SMART; SM00192; LDLa; 4.
DR   SMART; SM00281; LamB; 3.
DR   SMART; SM00282; LamG; 3.
DR   SMART; SM00200; SEA; 1.
DR   PROSITE; PS00022; EGF_1; 8.
DR   PROSITE; PS01186; EGF_2; 5.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 3.
DR   PROSITE; PS01209; LDLRA_1; 4.
DR   PROSITE; PS50068; LDLRA_2; 4.
DR   PROSITE; PS50024; SEA; 1.
KW   Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW   Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW   Extracellular matrix; EGF-like domain.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22   3707       BASEMENT MEMBRANE-SPECIFIC HEPARAN
FT                               SULFATE PROTEOGLYCAN CORE PROTEIN.
FT   DOMAIN      80    194       SEA.
FT   DOMAIN     195    234       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN     281    319       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN     320    359       LDL-RECEPTOR CLASS A 3.
FT   DOMAIN     360    403       LDL-RECEPTOR CLASS A 4.
FT   DOMAIN     404    504       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN     521    530       LAMININ EGF-LIKE 1 (N-TERMINAL).
FT   DOMAIN     531    730       LAMININ DOMAIN IV 1 (DOMAIN III A).
FT   DOMAIN     731    763       LAMININ EGF-LIKE 1 (C-TERMINAL).
FT   DOMAIN     764    813       LAMININ EGF-LIKE 2.
FT   DOMAIN     814    871       LAMININ EGF-LIKE 3.
FT   DOMAIN     879    923       LAMININ EGF-LIKE 4 (INCOMPLETE).
FT   DOMAIN     924    933       LAMININ EGF-LIKE 5 (N-TERMINAL).
FT   DOMAIN     934   1125       LAMININ DOMAIN IV 2 (DOMAIN III B).
FT   DOMAIN    1126   1158       LAMININ EGF-LIKE 5 (C-TERMINAL).
FT   DOMAIN    1159   1208       LAMININ EGF-LIKE 6.
FT   DOMAIN    1209   1265       LAMININ EGF-LIKE 7.
FT   DOMAIN    1275   1324       LAMININ EGF-LIKE 8.
FT   DOMAIN    1325   1334       LAMININ EGF-LIKE 9 (N-TERMINAL).
FT   DOMAIN    1335   1529       LAMININ DOMAIN IV 3 (DOMAIN III C).
FT   DOMAIN    1530   1562       LAMININ EGF-LIKE 9 (C-TERMINAL).
FT   DOMAIN    1563   1612       LAMININ EGF-LIKE 10.
FT   DOMAIN    1613   1670       LAMININ EGF-LIKE 11.
FT   DOMAIN    1677   1771       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN    1772   1865       IG-LIKE C2-TYPE DOMAIN 3.
FT   DOMAIN    1866   1954       IG-LIKE C2-TYPE DOMAIN 4.
FT   DOMAIN    1955   2049       IG-LIKE C2-TYPE DOMAIN 5.
FT   DOMAIN    2050   2148       IG-LIKE C2-TYPE DOMAIN 6.
FT   DOMAIN    2149   2244       IG-LIKE C2-TYPE DOMAIN 7.
FT   DOMAIN    2245   2343       IG-LIKE C2-TYPE DOMAIN 8.
FT   DOMAIN    2344   2436       IG-LIKE C2-TYPE DOMAIN 9.
FT   DOMAIN    2437   2532       IG-LIKE C2-TYPE DOMAIN 10.
FT   DOMAIN    2533   2619       IG-LIKE C2-TYPE DOMAIN 11.
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FT   DOMAIN     2620   2720       IG-LIKE C2-TYPE DOMAIN 12.
FT   DOMAIN     2721   2809       IG-LIKE C2-TYPE DOMAIN 13.
FT   DOMAIN     2810   2895       IG-LIKE C2-TYPE DOMAIN 14.
FT   DOMAIN     2896   2980       IG-LIKE C2-TYPE DOMAIN 15.
FT   DOMAIN     2984   3162       LAMININ G-LIKE 1.
FT   DOMAIN     3163   3241       EGF-LIKE.
FT   DOMAIN     3245   3425       LAMININ G-LIKE 2.
FT   DOMAIN     3518   3705       LAMININ G-LIKE 3.
FT   SITE         65     67       HEPARAN SULFATE (POTENTIAL).
FT   SITE         71     73       HEPARAN SULFATE (POTENTIAL).
FT   SITE         76     78       HEPARAN SULFATE (POTENTIAL).
FT   SITE       3615   3617       MEDIATES MOTOR NEURON ATTACHMENT
FT                                (POTENTIAL).
FT   DISULFID    199    212       BY SIMILARITY.
FT   DISULFID    206    225       BY SIMILARITY.
FT   DISULFID    219    234       BY SIMILARITY.
FT   DISULFID    285    297       BY SIMILARITY.
FT   DISULFID    292    310       BY SIMILARITY.
FT   DISULFID    304    319       BY SIMILARITY.
FT   DISULFID    325    337       BY SIMILARITY.
FT   DISULFID    332    350       BY SIMILARITY.
FT   DISULFID    344    359       BY SIMILARITY.
FT   DISULFID    368    381       BY SIMILARITY.
FT   DISULFID    375    394       BY SIMILARITY.
FT   DISULFID    388    403       BY SIMILARITY.
FT   DISULFID    428    479       BY SIMILARITY.
FT   DISULFID    764    773       BY SIMILARITY.
FT   DISULFID    766    780       BY SIMILARITY.
FT   DISULFID    783    792       BY SIMILARITY.
FT   DISULFID    795    811       BY SIMILARITY.
FT   DISULFID    814    829       BY SIMILARITY.
FT   DISULFID    816    839       BY SIMILARITY.
FT   DISULFID    842    851       BY SIMILARITY.
FT   DISULFID    854    869       BY SIMILARITY.
FT   DISULFID   1159   1168       BY SIMILARITY.
FT   DISULFID   1161   1175       BY SIMILARITY.
FT   DISULFID   1178   1187       BY SIMILARITY.
FT   DISULFID   1190   1206       BY SIMILARITY.
FT   DISULFID   1209   1224       BY SIMILARITY.
FT   DISULFID   1211   1234       BY SIMILARITY.
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FT   DISULFID   1249   1263       BY SIMILARITY.
FT   DISULFID   1275   1287       BY SIMILARITY.
FT   DISULFID   1277   1293       BY SIMILARITY.
FT   DISULFID   1295   1304       BY SIMILARITY.
FT   DISULFID   1307   1322       BY SIMILARITY.
FT   DISULFID   1563   1572       BY SIMILARITY.
FT   DISULFID   1565   1579       BY SIMILARITY.
FT   DISULFID   1582   1591       BY SIMILARITY.
FT   DISULFID   1594   1610       BY SIMILARITY.
FT   DISULFID   1613   1628       BY SIMILARITY.
FT   DISULFID   1615   1638       BY SIMILARITY.
FT   DISULFID   1641   1650       BY SIMILARITY.
FT   DISULFID   1653   1668       BY SIMILARITY.
FT   DISULFID   1792   1839       BY SIMILARITY.
FT   DISULFID   1886   1932       BY SIMILARITY.
FT   DISULFID   1976   2021       BY SIMILARITY.
FT   DISULFID   2073   2118       BY SIMILARITY.
FT   DISULFID   2170   2215       BY SIMILARITY.
FT   DISULFID   2268   2313       BY SIMILARITY.
FT   DISULFID   2365   2413       BY SIMILARITY.
FT   DISULFID   2456   2506       BY SIMILARITY.
FT   DISULFID   2554   2599       BY SIMILARITY.
FT   DISULFID   2641   2686       BY SIMILARITY.

  Query Match             3.7%;  Score 137.5;  DB 1;  Length 3707;
  Best Local Similarity   19.5%;  Pred. No. 0.034;
  Matches  163;  Conservative   73;  Mismatches  235;  Indels  365;  Gaps   42;

Qy       4 PWFLLSLALGRSPVVLSLERLVGPQDAT----HCSP----------------GLSC----  39
           | |||    | |          |||:|:    || |                 | |
Db     272 PQFLLPSVPGPS--------ACGPQEASCHSGHCIPRDYLCDGQEDCRDGSDELGCASPP 323

Qy      40 ----------------RLWDSDILCLPGDI-----------VPAPGPVLAPTHLQTELV  71
                           :|| |    ||            |  || |  ||| |
Db     324 PCEPNEFACENGHCALKLWRCD-----GDFDCEDRTDEANCSVKQPGEVCGPTHFQCVST 378

Qy      72 LR-------CQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNASLQAQ 124
           |       | :|:||                  |:  ::||      |  |:  |:||
Db     379 NRCIPASFHCDEESDC-----------------PDRSDEFGCMPPQVVTPPQQ-SIQA- 418

Qy     125 VVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKE 184
                                    ||   :| : |    : : :  |
Db     419 ------------------------SRGQ---TVTFTCVATGVPTPIINW---------R 441

Qy     185 LNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFG-------------------LSLYW 224
           ||    :|| | : ::::|    |::   :|   |                     | |
Db     442 LN-WGHIPAHPRVTMTSEGGRGTLIIRDVKEADQGAYTCEAMNSRGMVFGIPDGVLELV- 499

Qy     225 NQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICP----FREDPR 280
             | | |  | |        :    :|| | |          ||:|     ||:  |
Db     500 --PQRGPCPDGHFYLE-------DSASCLPCFCFGV---------TNVCQSSLRFRDQIR 541

Qy     281 A---HQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTV 337
             | ::   : :                                | || |||||   : :
Db     542 LSFDQPNDFKGVNVTM--------------------------PSQPGVPPLSSTQLQI 573

Qy     338 DKVL-EFPLLKGHPNLCVQVNSSEKLQLQECLWA----------DSLG------------ 374
           |  | || |          |: | :  : :  ||          || |
Db     574 DPALQEFQL----------VDLSRRFLVHDAFWALPKQFLGNKVDSYGGFLRYKVRYELA 623

Qy     375 -----PL-KDDVLL------LETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQ 422
                |: | ||:|      | :||                  |   : |  :| |
Db     624 RGMLEPVQKPDVILVGAGYRLHSRGHTPTH------------PGTLNQRQVQLSE---- 666

Qy     423 DLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFA-AALSLILLLKKDHAKAA 481
                                 : ::|:    |  | :| | |:|  :||    : | |
Db     667 ----------------------EHWVHESGRPVQRAEMLQALASLEAVLLQTVYNTKMA 703

Qy     482 ARGRAALLLYSADDSGFERLVGALASAL--CQLPLRVAVDLWSRRELSAQGPVAWFHAQR 539
           : | : :::   | :     :   | ::  |: |:  :         || :   | |
Db     704 SVGLSDIVM---DTTVTHTTIHGRAHSVEECRCPIGYS-------GLSCESCDAHF---- 749

Qy     540 RQTLQEGGVVVLLFS----PGAVALC------------SEWLQDGVSGPGAHGPHDAFR 582
             |  ||  :  |     |  : |                :|  |     ||  |  || :
Db     750 --TRVPGGPYLGTCSGCNCNGHASSCDPVYGHCLNCQHNTEGPQCDKCKPGFFG--DATK 805

Qy     583 ASLSCVLPDFLQGRAPGSYVGA-------CFDRLLHPDAVPALFRTVPVFT---LPSQLP 632
           |: :   |       |  |: |       ||   |  |          | :|     |  |
Db     806 ATATACRP------CPCPYIDASRRFSDTCF---LDTDGQATCDACAPGYTGRRCESCAP 856

Qy     633 DFLGALQQP------------RAPRSGRLQERAEQ-------VSRALQPALDSYFH 669
             : |   ||            |    | |    |       | |      |  ||
Db     857 GYEGNPIQPGGKCRPTTQEIVRCDERGSLGTSGETCRCKNNVVGRLCNECSDGSFH 912


RESULT 4
PTPO_RAT
ID   PTPO_RAT       STANDARD;      PRT;  1711 AA.
AC   Q64612;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Osteotesticular protein tyrosine phosphatase precursor (EC 3.1.3.48)
DE   (OST-PTP).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Osteosarcoma;
RX   MEDLINE=95074080; PubMed=7527035;
RA   Mauro L.J., Olmsted E.A., Skrobacz B.M., Mourey R.J., Davis A.R.,
RA   Dixon J.E.;
RT   "Identification of a hormonally regulated protein tyrosine
```

```
RT   phosphatase associated with bone and testicular differentiation.";
RL   J. Biol. Chem. 269:30659-30667(1994).
CC   -!- FUNCTION: MAY FUNCTION IN SIGNALING PATHWAYS DURING BONE
CC       REMODELING, AS WELL AS SERVE A BROADER ROLE IN CELL INTERACTIONS
CC       ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS. OPTIMAL PH FOR
CC       PHOSPHATASE ACTIVITY IS 5.6.
CC       ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
CC       produced by alternative splicing. A presumed alternate transcript
CC       of 4.8-5.0 kilobases, which may lack PTP domains, is present in
CC       proliferating osteoblasts, but not detectable at other stages.
CC   -!- TISSUE SPECIFICITY: BONE AND TESTIS. IN THE LATTER, RESTRICTED TO
CC       THE BASAL PORTION OF THE SEMINIFEROUS TUBULE.
CC   -!- DEVELOPMENTAL STAGE: UP-REGULATED IN DIFFERENTIATING CULTURES OF
CC       PRIMARY OSTEOBLASTS AND DOWN-REGULATED IN LATE STAGE MINERALIZING
CC       CULTURES. IN TESTIS, EXPRESSION IS HIGHEST BETWEEN STAGES I AND
CC       VII WHEN MATURING SPERMATIDS REMAIN BURIED WITHIN THE SERTOLI
CC       EPITHELIUM.
CC   -!- INDUCTION: BY PARATHYROID HORMONE AND CYCLIC AMP ANALOGS.
CC   -!- PTM: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION
CC       SITES.
CC   -!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 10 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L36884; AAA63911.1; -.
DR   HSSP; P18052; 1YFO.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00041; fn3; 7.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00014; FNTYPEIII.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00060; FN3; 6.
DR   SMART; SM00194; PTPc; 1.
DR   SMART; SM00012; PTPc_DSPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW   Hydrolase; Transmembrane; Repeat; Signal; Glycoprotein.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18   1711       OSTEOTESTICULAR PROTEIN TYROSINE
FT                                PHOSPHATASE.
FT   DOMAIN      18   1074       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM  1075   1095       POTENTIAL.
FT   DOMAIN    1096   1711       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      32    124       FIBRONECTIN TYPE-III 1.
FT   DOMAIN     125    215       FIBRONECTIN TYPE-III 2.
FT   DOMAIN     216    303       FIBRONECTIN TYPE-III 3.
FT   DOMAIN     304    392       FIBRONECTIN TYPE-III 4.
FT   DOMAIN     393    470       FIBRONECTIN TYPE-III 5.
FT   DOMAIN     471    562       FIBRONECTIN TYPE-III 6.
FT   DOMAIN     563    652       FIBRONECTIN TYPE-III 7.
FT   DOMAIN     653    741       FIBRONECTIN TYPE-III 8.
FT   DOMAIN     742    830       FIBRONECTIN TYPE-III 9.
FT   DOMAIN     831    921       FIBRONECTIN TYPE-III 10.
FT   DOMAIN    1150   1418       PROTEIN-TYROSINE PHOSPHATASE 1.
FT   DOMAIN    1419   1711       PROTEIN-TYROSINE PHOSPHATASE 2.
FT   ACT_SITE  1350   1350       BY SIMILARITY.
FT   CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    74     74       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   117    117       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   239    239       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   259    259       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   431    431       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   570    570       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   620    620       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   649    649       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   663    663       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   737    737       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   851    851       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   882    882       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   970    970       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   982    982       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE  1711 AA;  187292 MW;  0F04D2D1A47A18A0 CRC64;

  Query Match             3.2%;  Score 118.5;  DB 1;  Length 1711;
  Best Local Similarity  18.9%;  Pred. No. 0.4;
  Matches  151;  Conservative   81;  Mismatches  272;  Indels  293;  Gaps   37;

Qy       5 WFLLSLALG-RSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPVLAP 63
           |      || |   ||   :| || ::|      |                  ||| | |
Db     322 WASWKAGLGARDGYVL---KLSGPMESTSTLGPEECN-------------AVFPGP-LPP 364

Qy      64 THLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEE----PRNA 119
             |   :|                                 :   |  |: ||       :|
Db     365 GHYTLQL-------------------------------KVLAGPYDAWVEGSTWLAESA 392

Qy     120 SLQAQVV--------LSFQAYPTARCVLLEVQVPAALVQFGQSVGS--VVYDCFEAALGS 169
           :|  :|          |      |  | :|     | :|        |:  |::
Db     393 ALPREVPGARLWLDGLEASKQPGRRALLYSDDAPGSLGNISVPSGATHVIFCGLVPGAHY 452

Qy     170 EVRIWSYTQPRYEKELNHTQQLP--ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQV 227
           | | | |    :   :|  ||  :|  :: |:  |                 |:: |
Db     453 RVDIASSTGDISQSISGYTSPLPPQSLEVISRSSPSD--------------LTIAWGPA 497

Qy     228 QGP---PKPRWHKNLT----------GPQIITLNHTDLVP--CLCIQVWP----LEPDSV 268
           |     |  ||:: :          ||  ::|    |||  |  :  |     |: ||
Db     498 PGQLEGYKVTWHQDGSQRSPGDLVDLGPDTLSLTLKSLVPGSCYTVSAWAWAGNLDSDSQ 557

Qy     269 RTNICP----------FREDPRAHQNLW----------QAARLRLLTLQ-------- 297
           : : |           |   | | :  |          :  ||| |||:
Db     558 KIHSCTRPAPPTNLSLGFAHQPAALKASWYHPPGGRDAFHLRLYRLRPLTLESEKVLPRE 617

Qy     298 ----SWL-LDAPCSLPAEAALCW--------RAPGGDPCQPLVPPLSWENVTVDKVLEFP 344
               || | | |    : :  |          | |  |  |  | | |  ||| |   :
Db     618 AQNFSWAQLTAGCEFQVQLSTLWGSERSSSANATGWTP--PSAPTL--VNVTSDAPTQLQ 673

Qy     345 LLKGHPNLCVQVNSSEKLQLQECLWADS-------LGPLKDDVLLLETRGPQDNRSLCAL 397
           :   |          : : |  |: :|       :||             :|  |   |
Db     674 VSWAHV-------PGGRSRYQVTLYQESTRTATSIMGP-----------KEDGTSFLGL 714

Qy     398 EPS-----GCTSLPSKASTRAARLGEY--------LLQDLQSGQCLQLWDDDLGALWACP 444
           |          |     | || :  :          ||  :|:|  :
Db     715 TPGTKYKVEVISWAGPLYTAAANVSAWTYPLIPNELLVSMQAGSAVV------------ 761

Qy     445 MDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVGA 504
                 | | :  |   |          ||: :  |  :
Db     762 ---------NLAWPSGPLGQGAC---------HAQLSDAGHLS----------------- 786

Qy     505 LASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEG-GVVVLLFSPGAVALCSE 563
             : ||::  :|:  |:|:    ::      |   ||    :|||   || |
Db     787 -----WEQPLKLGQELFMLRDLTPGHTISMSVRCRAGPLQASTHLVVLSVEPGPV----- 836

Qy     564 WLQDGVSGPGAHGPHDAFRASLSCVLPD--------FLQGRAPGS------YVGACFDRL 609
             :| :  |       :|   :|:  :|          ::   ||        |    | |
Db     837 --EDVLCHP------EATYLALNWTMPAGDVDVCLVVVERLVPGGGTHFVFQVNTSGDAL 888

Qy     610 LHPDAVPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFH 669
           | |: :|     : :  |                  ||    :  ||      : ::: |
Db     889 LLPNLMPTTSYRLSLTVL------------------GRNSRWSRAVSLVCSTSAEAW-H 928
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Qy    670 PPGTPAP-----GRGVG 681
          ||     |     | |:|
Db    929 PPELAEPPQVELGTGMG 945


RESULT 5
PQQF_KLEPN
ID   PQQF_KLEPN     STANDARD;      PRT;   761 AA.
AC   P27508;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Coenzyme PQQ synthesis protein F (EC 3.4.99.-).
GN   PQQF.
OS   Klebsiella pneumoniae.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Klebsiella.
OX   NCBI_TaxID=573;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCTC 418;
RX   MEDLINE=92212293; PubMed=1313537;
RA   Meulenberg J.J.M., Sellink E., Riegman N.H., Postma P.W.;
RT   "Nucleotide sequence and structure of the Klebsiella pneumoniae pqq
RT   operon.";
RL   Mol. Gen. Genet. 232:284-294(1992).
CC   -!- FUNCTION: REQUIRED FOR COENZYME PYRROLO-QUINOLINE-QUINONE (PQQ)
CC       BIOSYNTHESIS. IT IS THOUGHT THAT THIS PROTEIN IS A PROTEASE THAT
CC       CLEAVES PEPTIDES BOND IN A SMALL PEPTIDE (GENE PQQA) WHICH WOULD
CC       PROVIDE THE GLUTAMATE AND TYROSINE RESIDUES WHICH ARE NECESSARY
CC       FOR THE SYNTHESIS OF PQQ.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X58778; CAA41584.1; -.
DR   PIR; S20458; S20458.
DR   MEROPS; M16.006; -.
DR   InterPro; IPR001431; Peptidase_M16.
DR   Pfam; PF00675; Peptidase_M16; 1.
DR   PROSITE; PS00143; INSULINASE; 1.
KW   PQQ; Hydrolase; Metalloprotease; Zinc.
FT   METAL       49     49       ZINC (BY SIMILARITY).
FT   ACT_SITE    52     52       BY SIMILARITY.
FT   METAL       53     53       ZINC (BY SIMILARITY).
FT   METAL      130    130       ZINC (BY SIMILARITY).
SQ   SEQUENCE   761 AA;  83616 MW;  187182DBC8E839B5 CRC64;

  Query Match             3.1%;  Score 113.5;  DB 1;  Length 761;
  Best Local Similarity   23.4%;  Pred. No. 0.35;
  Matches  117;  Conservative   50;  Mismatches  165;  Indels  167;  Gaps   27;

Qy    282 HQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGG---DPCQPLVPPLSWENVTVD 338
          |:  : | |::|     | |  | || |   |  |   |       |  |||
Db    182 HRTHYVARRMQL-----W-LQGPQSLEALGELAARFAAGLAAGEAPPPAPPL-------- 227

Qy    339 KVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALE 398
          :: ||  |:       : |:|      |  ||   |  | |:| ||
Db    228 RLGEFTALQ------LAVSS------QPALWRCPLIALSDNVTLLR-------------- 261

Qy    399 PSGCTSLPSKASTRAARLGEYLLQD----LQSGQCLQLWDDDLGALWACPMDKYIHKRWA 454
                          |:|| :    | :|   :    |:   |       :::
Db    262 ------------------EFLLDEAPGSLMAGLRQRRLAGDVALNW-------LYQDRH 295

Qy    455 LVWLACLLFAA---------------ALSLILLLKKDHAKAAARGRAALL---------- 489
          | ||| |:||:                ||      :: |    :| |   |
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Db    296 LGWLA-LVFASDRPEEVDRQITHWLQALQQTTPEQQQHYYQLSRRRFQALSPLDQLRQRA 354

Qy    490 ---LYSADDSGFERLVGAL-----ASALCQ--------------LPLRVAVDLWSRRELS 527
              |  :||      ||       |  ||                |||       | ||  |
Db    355 FGFAPGAPPAGFADFCAALQVAPSVSLACQTVSPGEPVATQGFSLPL----SRWRRRPES 410

Qy    528 AQGPVAWFHAQRRQTL-----QEGGVVVLLFSPG--------AVALCSEWLQDGVS---- 570
                |: |    |      ::   :: | |||             ||    :|::
Db    411 DPALAFAFYPQAAGDLVAKCPEKAAPLLHLPSPGDPPRLLLRPPFYCSPDQAEGLARGEQ 470

Qy    571 ---------GPGAHGPHDAFRAS--LSCVLPDFLQGRAPGSYVGACFDRLLHPDA--VPA 617
                  | ||    |  |  |:  ||:   || | : : |   :|  | |   |:
Db    471 LRPLLAALRHAGGHGEWHLFDGSWQLTLQLPE--PGRRPEAILQAILRQLALPVASLTPS 528

Qy    618 LFRTVPVFTLPSQLPDFLGALQQPR---APRSGRLQERAEQVSRALQPALDSYFHPPGTP 674
             :: :  | :|||: ||     :   |  :|   | |: |:| |   : :  :||  |
Db    529 P-ESIAIRHLMAQLPERLGTSGHQKGWLAALAGGSAEDAQWVARQLS-LITAPVNPP-MP 585

Qy    675 APG---RGVGPGAGPGAGD 690
          ||    |||      || ||
Db    586 APAPCRRGVERLVYPG-GD 603


RESULT 6
RCQ4_HUMAN
ID   RCQ4_HUMAN     STANDARD;      PRT;  1208 AA.
AC   O94761;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   ATP-dependent DNA helicase Q4 (RecQ protein-like 4).
GN   RECQL4 OR RECQ4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=99097344; PubMed=9878247;
RA   Kitao S., Ohsugi I., Ichikawa K., Goto M., Furuichi Y., Shimamoto A.;
RT   "Cloning of two new human helicase genes of the RecQ family:
RT   biological significance of multiple species in higher eukaryotes.";
RL   Genomics 54:443-452(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20021764; PubMed=10552928;
RA   Kitao S., Lindor N.M., Shiratori M., Furuichi Y., Shimamoto A.;
RT   "Rothmund-Thomson syndrome responsible gene, RECQL4: genomic structure
RT   and products.";
RL   Genomics 61:268-276(1999).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- DISEASE: DEFECTS IN RECQL4 ARE A CAUSE OF ROTHMUND-THOMSON
CC       SYNDROME (RTS). A DISEASE CHARACTERIZED BY DERMAROLOGICAL FEATURES
CC       SUCH AS ATROPHY, PIGMENTATION, AND TELANGIECTASIA AND FREQUENTLY
CC       ACCOMPANIED BY JUVENILE CATARACT, SADDLE NOSE, CONGENITAL BONE
CC       DEFECTS, DISTURBANCES OF HAIR GROWTH, AND HYPOGONADISM.
CC   -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/RECQL4ID285.html".
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB006532; BAA74453.1; -.
DR   EMBL; AB026546; BAA86899.1; -.
DR   Genew; HGNC:9949; RECQL4.
DR   MIM; 603780; -.
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DR   MIM; 268400; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR004589; RecQ.
DR   InterPro; IPR001878; Znf_CCHC.
DR   Pfam; PF00270; DEAD; 1.
DR   Pfam; PF00271; helicase_C; 1.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
DR   SMART; SM00343; ZnF_C2HC; 1.
DR   TIGRFAMs; TIGR00614; recq; 1.
KW   Hydrolase; Helicase; ATP-binding; Nuclear protein.
FT   NP_BIND     502    509       ATP (POTENTIAL).
FT   SITE        605    608       DEAH BOX.
SQ   SEQUENCE   1208 AA;  133076 MW;  CB809A7765AB48A1 CRC64;

  Query Match             3.0%; Score 112.5;  DB 1;  Length 1208;
  Best Local Similarity   19.6%;  Pred. No. 0.76;
  Matches  115;  Conservative   73;  Mismatches  194;  Indels  205;  Gaps   31;

Qy      16 PVVLSLERLVGPQDATHCSPGLSC---RLWDSDIL--CLPGDIVPAPGPVLAPTHLQ--- 67
           |  | : :::  :   ||  ||:    |   ||:       :     ||   ||:|
Db     619 PCYLRVCKVLRERMGVHCFLGLTATATRRTASDVAQHLAVAEEPDLHGPAPVPTNLHLSV 678

Qy      68 ----------------------TELVLRCQKETDCDLCLRVAVHL--AVHGHWEEPEDEE 103
                                  ::: | :  | :   |:|  |   :|  |
Db     679 SMDRDTDQALLTLLQGKRFQNLDSIIIYCNRREDTE---RIAALLRTCLHAAWVPGS--- 732

Qy     104 KFGGAADSGVEEPRNASL--------------QAQVVLSFQAY------PTARCVLLEV 142
             || |      |  :| :               | :||::  |:       |  | | | :
Db     733 --GGRAPKTTAEAYHAGMCSRERRRVQRAFMQGQLRVVVATVAFGMGLDRPDVRAV-LHL 789

Qy     143 QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYE--KELNHTQQLPALPWLNVS 200
           :| :   : |:||    |       |       : ||: |  :||      :  :| |
Db     790 GLPPSFESYVQAVGRAGRD------GQPAHCHLFLQPQGEDLRELRRHVHADSTDFLAVK 843

Qy     201 ADGDNVHLVLNV------------SEEQHFGLSLYWNQVQGP-PKPRW---------HKN 238
                ||  |              ||::          | |  | |::         |:
Db     844 ------RLVQRVFPACTCTCTRPPSEQE--------GAVGGERPVPKYPPQEAEQLSHQA 889

Qy     239 LTGPQIITLNHTDLVPC-LCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLL--T 295
           ||: : : |   :|  | :|   :  ::: | :|        | : |    | ||  |
Db     890 APGPRRVCMGHERALPIQLTVQALDMPEEAIETLLCYL----ELHPHHW----LELLATT 941

Qy     296 LQSWLLDAPCSLPAEAALCWRAP----------GGDPCQ----------PLVPPLSWENV 335
             |: |        ||  | |            || |            ||  : ||
Db     942 YTHCRLNCPGGPAQLQALAHRCPPLAVCLAQQLPEDPGQGSSSVEFDMVKLVDSMGWELA 1001

Qy     336 TVDKVL--------------------EFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
           :| : |                    ||  |  |      : : || |: : |:    |
Db    1002 SVRRALCQLQWDHEPRTGVRRGTGVLVEFSELAFHLRSPGDLTAEEKDQICDFLY----G 1057

Qy     375 PLKDDVLLLETRGPQDNRSLCALE----------PSGCTSLPSKASTRAAR----LGEY 419
           ::           :: ::|  |            ||    |  :   |: |    || |
Db    1058 RVQ----------ARERQALARLRRTFQAFHSVAFPSCGPCLEQQDEERSTRLKDLLGRY 1107

Qy     420 L----------LQDLQS---GQC-LQLWDDDLGALWACPMDKYIHKR 452
                      ::| |    ||  || |:| :     | : :::  |
Db    1108 FEEEEGQEPGGMEDAQGPEPGQARLQDWEDQV----RCDIRQFLSLR 1150


RESULT 7
W70T_HUMAN
ID   W70T_HUMAN     STANDARD;      PRT;   925 AA.
AC   P57737;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   70 kDa WD-repeat tumor rejection antigen homolog.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA   Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC   -!- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK025674; BAB15211.1; -.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 6.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   ProDom; PD000018; WD40; 2.
DR   SMART; SM00320; WD40; 6.
DR   PROSITE; PS00678; WD_REPEATS_1; 1.
DR   PROSITE; PS50082; WD_REPEATS_2; 4.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW   Repeat; WD repeat.
FT   REPEAT       75    115       WD 1.
FT   REPEAT      124    163       WD 2.
FT   REPEAT      166    205       WD 3.
FT   REPEAT      209    253       WD 4.
FT   REPEAT      542    582       WD 5.
FT   REPEAT      592    632       WD 6.
FT   REPEAT      635    674       WD 7.
FT   REPEAT      728    768       WD 8.
SQ   SEQUENCE   925 AA;  100574 MW;  A393CE973C94F4A9 CRC64;

  Query Match             2.9%;  Score 108.5;  DB 1;  Length 925;
  Best Local Similarity   21.7%;  Pred. No. 1.1;
  Matches  134;  Conservative   53;  Mismatches  223;  Indels  207;  Gaps   31;

Qy      10 LALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTE 69
           || | :   : | || ||  |                    ||     ||| || |  |  |
Db      93 LATGSADRTVKLWRLPGPGQA-----------------LPS----APGVVLGPEDLPVE 130

Qy      70 LVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNASLQAQVVLSF 129
             ||:    :|  |       : |   |              |:  ::|
Db     131 -VLQFHPTSDGILVSAAGTTVKV---W------------DAAKQQP------------- 160

Qy     130 QAYPTARCVLLEVQVPAALVQF------GQSVGSVVYDCFEAALGSEVRIWS-YTQPRYE 182
                 | |:     |||       |  ||:   |         ::||:  |:||
Db     161 ---------LTELAAHGDLVQSAVWSRDGALVGTACKD-------KQLRIFDPRTKPRAS 204

Qy     183 K--ELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
           :  : :   :   | |:     |  |||           |  :||::     |
Db     205 QSTQAHENSRDSRLAWM-----GTWEHLV----------STGFNQMREREVKLWDTRFF 248

Qy     241 GPQIITLNHTDLVPCL--------------------CIQVWPLEPDSVRTNICPFRE- 277
           : :|     : ||                      | :| | :|       |
Db     249 SSALASLTLDTSLGCLVPLLDPDSGLLVLAGKGERQLYCYEVVPQQPALSPVTQCVLESV 308

Qy     278 ------DPRAHQNLWQAARLRLLTL-QSWLLDAPCSLPAEAALCWR--APGGDPCQPLVP 328
                ||    :    ||:| |  : ::     :| :|        |    | |
Db     309 LRGAALVPRQALAVMGCEVLRVLQLSDTAIVPIGYHVPRKAVEFHEDLFPDTAGCVPATD 368

Qy     329 PLSW---ENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDV--LLL 383
           |  |   :|  | ||   |  : ||:                ||      || |     ::
Db     369 PHGWWAGDNQQVQKVSLNPACRPHPS-----------FTSCL-VPPAEPLPDTAQPAVM 415

Qy     384 ETR-GPQDNRSLCALEPSGCTSLPSKASTRAARL----GEYLLQDLQSGQCLQLWDDDLG 438
           ||  |  |     :  ||  || ||  |:     |     |       |:| | |     ||
Db     416 ETPVGDADASEGFSSPPSSLTS-PSTPSSLGPSLSSTSGIGTSPSLRSLQSL------LG 468
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Qy     439 ALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGF 498
                 |  |: | :                    :| :|      :|    |    :  ||
Db     469 -----PSSKFRHAQGT----------------VLHRDSHITNLKG--LNLTTPGESDGF 504

Qy     499 ERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQR--------RQTLQEGGVVV 550
                   |   ||||| |     ||: | ||    ::          ||| |  |
Db     505 ----------CANKLRVAVPL-----LSSGGQVAVLELRKPGRLPDTALPTLQNGAAVT 548

Qy     551 LL----FSPGAVALCSE 563
             |    | |  :|:  |
Db     549 DLAWDPFDPHRLAVAGE 565


RESULT 8
IL4R_HUMAN
ID   IL4R_HUMAN     STANDARD;      PRT;   825 AA.
AC   P24394; Q96P01;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124
DE   antigen).
GN   IL4R OR IL4RA OR 582J2.1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=90171849; PubMed=2307934;
RA   Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V.,
RA   Gimpel S.D., Din W.S., Grabstein K.H., Widmer M.B., Park L.S.,
RA   Cosman D., Beckmann M.P.;
RT   "Human interleukin 4 receptor confers biological responsiveness and
RT   defines a novel receptor superfamily.";
RL   J. Exp. Med. 171:861-873(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91120547; PubMed=2278997;
RA   Galizzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O.,
RA   Kastelein R., Banchereau J., Howard M., Miyajima A.;
RT   "Molecular cloning of a cDNA encoding the human interleukin 4
RT   receptor.";
RL   Int. Immunol. 2:669-675(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99425270; PubMed=10493829;
RA   Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
RA   Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA   Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA   Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT   "Genome duplications and other features in 12 Mb of DNA sequence from
RT   human chromosome 16p and 16q.";
RL   Genomics 60:295-308(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
RX   MEDLINE=97224413; PubMed=9070874;
RA   Deichmann K., Bardutzky J., Forster J., Heinzmann A., Kuehr J.;
RT   "Common polymorphisms in the coding part of the IL4-receptor gene.";
RL   Biochem. Biophys. Res. Commun. 231:696-697(1997).
RN   [6]
RP   VARIANT ATOPIC ARG-576.
RX   MEDLINE=98041803; PubMed=9392697;
RA   Hershey G.K.K., Friedrich M.F., Esswein L.A., Thomas M.L.,
RA   Chatila T.A.;
RT   "The association of atopy with a gain-of-function mutation in the
RT   alpha subunit of the interleukin-4 receptor.";
RL   New Engl. J. Med. 337:1720-1725(1997).
RN   [7]
RP   VARIANT ATOPIC ASTHMA VAL-75.
RX   MEDLINE=98282087; PubMed=9620765;
RA   Mitsuyasu H., Izuhara K., Mao X.-Q., Gao P.S., Arinobu Y., Enomoto T.,
RA   Kawai M., Sasaki S., Dake Y., Hamasaki N., Shirakawa T., Hopkin J.M.;
RT   "Ile50Val variant of IL4R alpha upregulates IgE synthesis and
RT   associates with atopic asthma.";
RL   Nat. Genet. 19:119-120(1998).
RN   [8]
RP   VARIANT ATOPIC ASTHMA VAL-75.
RX   MEDLINE=99322293; PubMed=10390422;
RA   Noguchi E., Shibasaki M., Arinami T., Takeda K., Yokouchi Y.,
RA   Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi H.;
RT   "No association between atopy/asthma and the Ile50Val polymorphism of
RT   IL-4 receptor.";
RL   Am. J. Respir. Crit. Care Med. 160:342-345(1999).
RN   [9]
RP   VARIANTS PRO-503 AND ARG-576.
RX   MEDLINE=99250314; PubMed=10233717;
RA   Kruse S., Japha T., Tedner M., Sparholt S.H., Forster J., Kuehr J.,
RA   Deichmann K.A.;
RT   "The polymorphisms S503P and Q576R in the interleukin-4 receptor alpha
RT   gene are associated with atopy and influence the signal
RT   transduction.";
RL   Immunology 96:365-371(1999).
RN   [10]
RP   VARIANT ALA-752.
RX   MEDLINE=20143377; PubMed=10677312;
RA   Ober C., Leavitt S.A., Tsalenko A., Howard T.D., Hoki D.M., Daniel R.,
RA   Newman D.L., Wu X., Parry R., Lester L.A., Solway J., Blumenthal M.,
RA   King R.A., Xu J., Meyers D.A., Bleecker E.R., Cox N.J.;
RT   "Variation in the interleukin 4-receptor alpha gene confers
RT   susceptibility to asthma and atopy in ethnically diverse
RT   populations.";
RL   Am. J. Hum. Genet. 66:517-526(2000).
RN   [11]
RP   VARIANT ATOPIC ARG-576.
RX   MEDLINE=20269830; PubMed=10809862;
RA   Oiso N., Fukai K., Ishii M.;
RT   "Interleukin 4 receptor alpha chain polymorphism Gln551Arg is
RT   associated with adult atopic dermatitis in Japan.";
RL   Br. J. Dermatol. 142:1003-1006(2000).
RN   [12]
RP   VARIANT PRO-786.
RX   MEDLINE=21405389; PubMed=11513543;
RA   Andrews R.P., Burrell L., Rosa-Rosa L., Cunningham C.M.,
RA   Brzezinski J.L., Bernstein J.A., Khurana Hershey G.K.;
RT   "Analysis of the Ser786Pro interleukin-4 receptor alpha allelic
RT   variant in allergic and nonallergic asthma and its functional
RT   consequences.";
RL   Clin. Immunol. 100:298-304(2001).
RN   [13]
RP   VARIANT ILE-579.
RX   MEDLINE=21182061; PubMed=11285129;
RA   Lozano F., Places L., Vila J.M., Padilla O., Arman M., Gimferrer I.,
RA   Suarez B., Lopez de la Iglesia A., Miserachs N., Vives J.;
RT   "Identification of a novel single-nucleotide polymorphism (Val554Ile)
RT   and definition of eight common alleles for human IL4RA exon 11.";
RL   Tissue Antigens 57:216-220(2001).
CC   -!- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-4. A SOLUBLE FORM
CC       OF THE IL-4 RECEPTOR MAY REPRESENT A REGULATORY MOLECULE SPECIFIC
CC       FOR IL-4-DEPENDENT IMMUNE RESPONSES.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DISEASE: DEFECTS IN IL4R ARE A CAUSE OF ATOPIC ASTHMA.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD124 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd124.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X52425; CAA36672.1; -.
DR   EMBL; AC004525; AAC23495.1; -.
DR   EMBL; AF421855; AAL12163.1; -.
DR   PIR; A60386; A60386.
DR   PIR; A47603; A47603.
DR   Genew; HGNC:6015; IL4R.
DR   MIM; 147781; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003531; Hemtopoptn_S_F1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;
KW   Polymorphism.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    825       INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
FT   DOMAIN       26    232       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    233    256       POTENTIAL.
FT   DOMAIN      257    825       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     34     44       BY SIMILARITY.
FT   DISULFID     74     86       BY SIMILARITY.
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    128    128       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    176    176       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    209    209       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      75     75       I -> V (IN ATOPIC ASTHMA).
FT                                /FTId=VAR_008034.
FT   VARIANT     400    400       E -> A (IN DBSNP:1805011).
FT                                /FTId=VAR_011657.
FT   VARIANT     431    431       C -> R (IN DBSNP:1805012).
FT                                /FTId=VAR_011658.
FT   VARIANT     436    436       S -> L (IN DBSNP:1805013).
FT                                /FTId=VAR_011659.
FT   VARIANT     503    503       S -> P (IN DBSNP:1805015).
FT                                /FTId=VAR_011660.
FT   VARIANT     576    576       Q -> R (IN ATOPIC PATIENTS).
FT                                /FTId=VAR_008035.
FT   VARIANT     579    579       V -> I.
FT                                /FTId=VAR_011661.
FT   VARIANT     752    752       S -> A (IN DBSNP:1805016).
FT                                /FTId=VAR_011662.
FT   VARIANT     786    786       S -> P (IN 1.8% OF THE POPULATION; IN
FT                                DBSNP:1805014).
FT                                /FTId=VAR_011663.
SQ   SEQUENCE   825 AA;  89658 MW;  9F886DF5612297F8 CRC64;

  Query Match             2.9%;  Score 107;  DB 1;  Length 825;
  Best Local Similarity   19.2%;  Pred. No. 1.3;
  Matches  155;  Conservative   66;  Mismatches  284;  Indels  304;  Gaps   36;

Qy      41 LWDSDILCLPGDIVP-------APGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVH 93
           ||    |   |   |       ||| :   |::   |:|        |  |   :  ||:
Db     103 LWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN 162

Qy      94 GHWEEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLE--VQVPAALVQF 151
             | | :  :                          |: |       ||  ::: |: ::
Db     163 -IWSENDPAD-----------------------FRIY---NVTYLEPSLRIAASTLKS 193

Qy     152 GQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLN 211
           | |             : || |:            ::  |:  | |   :    ||:|
Db     194 GIS-----------YRARVRAWAQCY-----NTTWSEWSPSTKWHNSYREPFEQHLLLG 236

Qy     212 VSEEQHFGLSL-------------YWNQVQGPPKPR------------WHKNLTGPQI 244
           ||      |::              :|:|:  | : |             | |   | :
Db     237 VSVSCIVILAVCLLCYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQEP 296

Qy     245 ITLNH-----TDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSW 299
             |     | |:||       || :  |       |||       :||  : :  |
Db     297 AKCPHWKNCLTKLLPCF------LEHNMKRD------EDPH------KAA--KEMPFQGS 336

Qy     300 LLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL----------LKGH 349
             | | :    : |             | |   |   :: | |:            ||
Db     337 GKSAWCPVEISKTVLW------------PESISVVRCVELFEAPVECEEEEEVEEEKG- 382

Qy     350 PNLCVQVNSSEK----------LQLQECLWADSLGPLKDDVLLLETRG---PQDNRSLCA 396
            : |    ||             :| | |: | ||         |  |    ||    |
Db     383 -SFCASPESSRDDFQEGREGIVARLTESLFLDLLG---------EENGGFCQQDMGESCL 432

Qy     397 LEPSGCTS-------LPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYI 449
           | ||| ||         ||      |   |:          | | |       :    | :
Db     433 LPPSGSTSAHMPWDEFPSAGPKEAPPWGK--------EQPLHLEPSPPASPTQSPDN--- 481

Qy     450 HKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVGALASAL 509
                 | |                                 |  | :  :     :|: :
Db     482 --------LTC-------------------------TETPLVIAGNPAYRSFSNSLSQSP 508

Qy     510 CQLPLRVAVDLWSRRELS-------------------AQGPVAWFHAQRRQTLQEGGVVV 550
           |  |  :  |     | |                   |  |    ||  || | |
Db     509 C--PRELGPDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNVLQHGAAAA 566

Qy     551 LLFSP--GAVALCSEWLQDGVS-------GPGAHGPHDAFRASL--SCVLPDFLQ-GRAP 598
            : :|  |          | |          ||     : || : |  | | |:    | :
Db     567 PVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAGYKAFSSLLASSAVSPEKCGFGASS 626

Qy     599 GSYVGACFDRLL-----HPDAVPALFRTVPVFT--------------LPSQLPDFLGA- 637
           |       |  |:       |  ||     ||:||               |||  |: ||
Db     627 GEEGYKPFQDLIPGCPGDPAPVP-----VPLFTFGLDREPPRSPQSSHLPSSSPEHLGLE 681

Qy     638 -------LQQPRAPRS----------------------GRLQERAEQVSRALQPALDS 666
                  : :|  |:                       | |::   |      | : |
Db     682 PGEKVEDMPKPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGGQTPVMAS 741

Qy     667 ---------YFHPPGTPAPGRGVGPGAGP 686
                      || ||       ||  |
Db     742 PCCGCCCGDRSSPPTTPLRAPDPSPGGVP 770


RESULT 9
NTC4_HUMAN
ID   NTC4_HUMAN     STANDARD;      PRT;  2003 AA.
AC   Q99466; O00306; Q99940; Q99458; Q9H3S8; Q9UII9; Q9UIJ0;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Neurogenic locus notch homolog protein 4 precursor (Notch 4)
DE   (hNotch4).
GN   NOTCH4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.
RC   TISSUE=Placenta;
RX   MEDLINE=97311416; PubMed=9168133;
RA   Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T.,
RA   Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;
RT   "Gene organization of human NOTCH4 and (CTG)n polymorphism in this
RT   human counterpart gene of mouse proto-oncogene Int3.";
RL   Gene 189:235-244(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC   TISSUE=Bone marrow, and Heart;
RX   MEDLINE=98360091; PubMed=9693032;
RA   Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,
RA   Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;
RT   "Cloning, characterization, and the complete 56.8-kilobase DNA
RT   sequence of the human NOTCH4 gene.";
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RL   Genomics 51:45-58(1998).
RN   [3]
RP   SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.
RA   Miyagawa T., Tokunaga K., Hojho H.;
RT   "Human notch4 gene variant.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   IDENTIFICATION OF LIGANDS.
RX   MEDLINE=99180765; PubMed=10079256;
RA   Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA   Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT   "Human ligands of the Notch receptor.";
RL   Am. J. Pathol. 154:785-794(1999).
CC   -!- FUNCTION: Functions as a receptor for membrane-bound ligands
CC       Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
CC       Upon ligand activation through the released notch intracellular
CC       domain (NICD) it forms a transcriptional activator complex with
CC       RBP-J kappa and activates genes of the enhancer of split locus.
CC       Affects the implementation of differentiation, proliferation and
CC       apoptotic programs. May regulate branching morphogenesis in the
CC       developing vascular system (By similarity).
CC   -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC       terminal fragment N(EC) which are probably linked by disulfide
CC       bonds (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC       proteolytical processing NICD is translocated to the nucleus.
CC   -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be
CC       produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in
CC       the lung and placenta and at low levels in the liver, skeletal
CC       muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow
CC       and fetal liver. No expression was seen in adult brain or
CC       peripheral blood leukocytes.
CC   -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC       which is proteolytically cleaved by a furin-like convertase in the
CC       trans-Golgi network before it reaches the plasma membrane to yield
CC       an active, ligand-accessible form. Cleavage results in a C-
CC       terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC       ligand binding, it is cleaved by TNF-alpha converting enzyme
CC       (TACE) to yield a membrane-associated intermediate fragment called
CC       notch extracellular truncation (NEXT). This fragment is then
CC       cleaved by presenilin dependent gamma-secretase to release a
CC       notch-derived peptide containing the intracellular domain (NICD)
CC       from the membrane (By similarity).
CC   -!- PTM: Phosphorylated (By similarity).
CC   -!- POLYMORPHISM: The poly-Leu region of NOTCH4 (in the signal
CC       peptide) is polymorphic and the number of Leu varies in the
CC       population (from 6 to 12).
CC   -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC   -!- SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC   -!- SIMILARITY: CONTAINS 5 ANK REPEATS.
CC   -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
CC       in position 1438 to 1463.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D63395; BAA09708.1; ALT_FRAME.
DR   EMBL; D86566; BAA13116.1; -.
DR   EMBL; U95299; AAC32288.1; -.
DR   EMBL; U89335; AAC63097.1; -.
DR   EMBL; AB023961; BAB20317.1; -.
DR   EMBL; AB024520; BAA88951.1; -.
DR   EMBL; AB024578; BAA88952.1; -.
DR   HSSP; P08709; 1BF9.
DR   Genew; HGNC:7884; NOTCH4.
DR   MIM; 164951; -.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR000800; Notch.
DR   Pfam; PF00008; EGF; 26.
DR   Pfam; PF00023; ank; 6.
DR   Pfam; PF00066; notch; 2.
DR   PRINTS; PR00010; EGFBLOOD.
DR   PRINTS; PR00011; EGFLAMININ.
DR   PRINTS; PR00012; FNTYPEI.
DR   SMART; SM00248; ANK; 5.
DR   SMART; SM00179; EGF_CA; 11.
DR   SMART; SM00001; EGF_like; 15.
DR   SMART; SM00004; NL; 2.
DR   PROSITE; PS50088; ANK_REPEAT; 5.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 11.
DR   PROSITE; PS00022; EGF_1; 28.
DR   PROSITE; PS01186; EGF_2; 21.
DR   PROSITE; PS01187; EGF_CA; 9.
KW   Receptor; Transcription regulation; Activator; Differentiation;
KW   Developmental protein; Repeat; ANK repeat; EGF-like domain;
KW   Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
KW   Triplet repeat expansion; Alternative splicing.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24   2003       NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 4.
FT   CHAIN     1432   2003       NOTCH EXTRACELLULAR TRUNCATION (BY
FT                               SIMILARITY).
FT   CHAIN     1467   2003       NOTCH INTRACELLULAR DOMAIN (BY
FT                               SIMILARITY).
FT   DOMAIN      24   1447       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM  1448   1468       POTENTIAL.
FT   DOMAIN    1469   2003       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      24     63       EGF-LIKE 1.
FT   DOMAIN      64    115       EGF-LIKE 2.
FT   DOMAIN     118    155       EGF-LIKE 3.
FT   DOMAIN     156    192       EGF-LIKE 4.
FT   DOMAIN     194    232       EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     234    274       EGF-LIKE 6.
FT   DOMAIN     276    312       EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     314    353       EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     355    391       EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     392    430       EGF-LIKE 10.
FT   DOMAIN     432    473       EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     475    511       EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     513    549       EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     551    587       EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     589    625       EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     626    659       EGF-LIKE 16.
FT   DOMAIN     661    689       EGF-LIKE 17.
FT   DOMAIN     691    727       EGF-LIKE 18.
FT   DOMAIN     729    765       EGF-LIKE 19.
FT   DOMAIN     767    803       EGF-LIKE 20.
FT   DOMAIN     806    842       EGF-LIKE 21.
FT   DOMAIN     844    880       EGF-LIKE 22.
FT   DOMAIN     882    928       EGF-LIKE 23.
FT   DOMAIN     930    966       EGF-LIKE 24.
FT   DOMAIN     968   1004       EGF-LIKE 25.
FT   DOMAIN    1006   1044       EGF-LIKE 26.
FT   DOMAIN    1046   1085       EGF-LIKE 27.
FT   DOMAIN    1087   1126       EGF-LIKE 28.
FT   DOMAIN    1130   1171       EGF-LIKE 29.
FT   DOMAIN    1472   1476       POLY-ARG.
FT   REPEAT    1165   1212       LIN/NOTCH 1.
FT   REPEAT    1213   1246       LIN/NOTCH 2.
FT   REPEAT    1247   1286       LIN/NOTCH 3.
FT   REPEAT    1633   1665       ANK 1.
FT   REPEAT    1666   1698       ANK 2.
FT   REPEAT    1700   1732       ANK 3.
FT   REPEAT    1733   1765       ANK 4.
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FT   REPEAT     1766   1798       ANK 5.
FT   DISULFID     28     41       BY SIMILARITY.
FT   DISULFID     35     51       BY SIMILARITY.
FT   DISULFID     53     62       BY SIMILARITY.
FT   DISULFID     68     80       BY SIMILARITY.
FT   DISULFID     74    103       BY SIMILARITY.
FT   DISULFID    105    114       BY SIMILARITY.
FT   DISULFID    122    133       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    145    154       BY SIMILARITY.
FT   DISULFID    160    171       BY SIMILARITY.
FT   DISULFID    165    180       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    198    211       BY SIMILARITY.
FT   DISULFID    205    220       BY SIMILARITY.
FT   DISULFID    222    231       BY SIMILARITY.
FT   DISULFID    238    249       BY SIMILARITY.
FT   DISULFID    243    262       BY SIMILARITY.
FT   DISULFID    264    273       BY SIMILARITY.
FT   DISULFID    280    291       BY SIMILARITY.
FT   DISULFID    285    300       BY SIMILARITY.
FT   DISULFID    302    311       BY SIMILARITY.
FT   DISULFID    318    332       BY SIMILARITY.
FT   DISULFID    326    341       BY SIMILARITY.
FT   DISULFID    343    352       BY SIMILARITY.

  Query Match           2.9%;  Score 107;  DB 1;  Length 2003;
  Best Local Similarity  21.8%;  Pred. No. 4;
  Matches  176;  Conservative   62;  Mismatches  251;  Indels  320;  Gaps   46;

Qy      32 HCSPGLSCRL----WDSDILCLPGDIVPAPGP------VLAPTHLQTELVLRCQKETDCD 81
           ||  |  |      ||    | | |  |  ||      ||:|  |  :|    :
Db    1267 HCEKG--CNTAECGWDGGD-CRPEDGDPEWGPSLALLVVLSPPALDQQLFALARV---LS 1320

Qy      82 LCLRVAVHLAVHGHWEEPE-------------DEEKFGGAADSGVEEPRNASLQAQ--- 124
           | |||       | |   :                |||  ||  |   :|   |: | |
Db    1321 LTLRV-------GLWVRKDRDGRDMVYPYPGARAEEKLGGTRDPTYQE--RAAPQTQPLG 1371

Qy     125 -----------VVLSFQA------YPTARCV----------------LLEVQVPAALVQ 150
                      ||:          :| :||                ||  :|  |:
Db    1372 KETDSLSAGFVVVMGVDLSRCGPDHPASRCPWDPGLLLRFLAAMAAVGALEPLLPGPLLA 1431

Qy     151 FGQSVG-------------SVVYDCFEAALGSEV-------------RIW---SYTQPR 180
                 |             | |      |||: :                :|    :|:
Db    1432 VHPHAGTAPPANQLPWPVLCSPVAGVILLALGALLVLQLIRRRRREHGALWLPPGFTRRP 1491

Qy     181 YEKELNHTQQLP------ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPK-- 232
             :  | :: |       |  |   |: |   :|:    |:  |  :   :  |||
Db    1492 RTQSAPHRRRPPLGEDSIGLKALKPKAEVDEDGVVMCSGPEE--GEEVGQAEETGPPSTC 1549

Qy     233 ------------------PRWHKNLTGPQIITLNHTDLVPCL----CIQV--------W 261
                            |   :  | : |     : | :    | :|         |
Db    1550 QLWSLSGGCGALPQAAMLTPPQESEMEAPDLDTRGPDGVTPLMSAVCCGEVQSGTFQGAW 1609

Qy     262 -----PLEPDSVRTNICPFREDPRAH------QNLWQAARLRLLTLQSWLLDAPCSLPAE 310
               | ||  :    |     |:||         |  |||    |    ||:|
Db    1610 LGCPEPWEP-LLDGGAC-----PQAHTVGTGETPLHLAARFSRPTAARRLLEA------- 1656

Qy     311 AALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWA 370
                 | :| ||              |:    ||     :  |  :: |  |
Db    1657 --------GANPNQP-----------DRAGRTPL-----HAAVAADAREVCQ------- 1684

Qy     371 DSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLG-EYLLQDLQSGQC 429
                  ||| :|      :: |    | | |       ||||  | |:::| : |
Db    1685 ----------LLLRSR----QTAVDARTEDGTTPL-----MLAARLAVEDLVEELIAAQA 1725

Qy     430 LQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALL 489
                |:||      ||:   : || | | :  | |   :|    |       | :  |
Db    1726 ------DVGA-----RDKW--GKTALHWAAAVNNARAARSLLQAGADKDAQDNREQTPLF 1772

Qy     490 LYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQ----TLQE 545
           | : :       ||:  |  | |  | :|   |: :   |    | ||      || |
Db    1773 LAARE--------GAVEVAQLLLGLGAAREL---RDQAGLAPADVAH-QRNHWDLLTLLE 1820

Qy     546 GGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGAC 605
           |                          :||                   |:      ||   |
Db    1821 G-----------------------AGP-----------------PEARHKATPGREAGP- 1839

Qy     606 FDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQQPR------APRSGR--LQERAEQVS 657
           | |             ||| |    |  |   ||| : |       || |   || |   |
Db    1840 FPRA----------RTVSV----SVPPHGGGALPRCRTLSAGAGPRGGGACLQARTWSVD 1885

Qy     658 RALQPALDSYFHPPGTPAPGRGVGPGAGP 686
           | :    :| |         ||| | ||
Db    1886 LAARGG-GAYSHCRSL----SGVGAGGGP 1909


RESULT 10
CUT1_CANFA
ID   CUT1_CANFA     STANDARD;      PRT;   975 AA.
AC   P39881;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   CCAAT displacement protein (Homeobox protein Clox) (Clox-1)
DE   (Fragment).
GN   CUTL1 OR CLOX.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart ventricle;
RX   MEDLINE=93161940; PubMed=1363085;
RA   Andres V., Nadal-Ginard B., Mahdavi V.;
RT   "Clox, a mammalian homeobox gene related to Drosophila cut, encodes
RT   DNA-binding regulatory proteins differentially expressed during
RT   development.";
RL   Development 116:321-334(1992).
CC   -!- FUNCTION: DNA-BINDING REGULATORY PROTEIN, WHERE THE SMALLER
CC       PROTEIN SPECIES PROBABLY REPRESENTS THE ACTIVE DNA-BINDING FORM.
CC       MAY FUNCTION AS A DEVELOPMENTALLY REGULATED REPRESSOR OF TISSUE-
CC       SPECIFIC GENE TRANSCRIPTION BY PREVENTING THE INTERACTION OF
CC       TISSUE-SPECIFIC TRANSACTIVATORS WITH THEIR COGNATE TARGET
CC       SEQUENCES. PROBABLY INVOLVED IN CELL-FATE SPECIFICATION IN DIVERSE
CC       DIFFERENTIATION PROGRAMS.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- ALTERNATIVE PRODUCTS: A number of isoforms may be produced by
CC       alternative splicing.
CC   -!- TISSUE SPECIFICITY: A BROAD PATTERN OF EXPRESSION OBSERVED IN
CC       TISSUES OF DIVERSE ORIGINS, SUCH AS CARTILAGE, LIVER, BRAIN, LUNG,
CC       HEART AND SKELETAL MUSCLE. THERE ARE 2 DISTINCT PROTEIN SPECIES:
CC       THE LARGER ONE (230-250 KDA) IS FOUND MAINLY IN ADULT BRAIN, LUNG
CC       AND HEART, AND THE SMALLER ONE (180-190 KDA) PREDOMINATES IN EARLY
CC       EMBRYONIC TISSUES.
CC   -!- DEVELOPMENTAL STAGE: DIFFERENTIALLY EXPRESSED DURING DEVELOPMENT.
CC       SMALL PROTEIN SPECIES PREDOMINATE IN EARLY EMBRYOS AND ARE
CC       UPREGULATED IN COMMITTED MYOBLASTS AND CHONDROCYTES, BUT
CC       DOWN-REGULATED UPON TERMINAL DIFFERENTIATION. LARGE SPECIES ARE
CC       DETECTED MAINLY IN ADULT TISSUES AND TERMINALLY DIFFERENTIATED
CC       CELLS.
CC   -!- DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIPATE IN
CC       REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND
CC       HETERODIMERIZATION.
CC   -!- SIMILARITY: CONTAINS 3 CUT DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CUT HOMEOBOX FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   EMBL; X69017; CAA48782.1; -.
DR   PIR; S33121; S33121.
DR   HSSP; P10037; 1AU7.
DR   TRANSFAC; T01485; -.
DR   TRANSFAC; T01995; -.
DR   InterPro; IPR003350; Hmoeo_CUT.
DR   InterPro; IPR001356; Homeobox.
DR   Pfam; PF00046; homeobox; 1.
DR   Pfam; PF02376; CUT; 3.
DR   ProDom; PD000010; Homeobox; 1.
DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
KW   Transcription regulation; Homeobox; DNA-binding;
KW   Developmental protein; Nuclear protein; Repeat; Repressor;
KW   Coiled coil; Alternative splicing.
FT   NON_TER       1      1
FT   DNA_BIND     <1     67       CUT 1.
FT   DOMAIN      113    169       COILED COIL (POTENTIAL).
FT   DNA_BIND    374    461       CUT 2.
FT   DNA_BIND    557    644       CUT 3.
FT   DNA_BIND    684    743       HOMEOBOX.
SQ   SEQUENCE   975 AA;  105428 MW;  724243B32C5BCFD9 CRC64;

  Query Match             2.8%;  Score 104.5;  DB 1;  Length 975;
  Best Local Similarity   20.4%;  Pred. No. 2.5;
  Matches  174;  Conservative   74;  Mismatches  244;  Indels  363;  Gaps   44;

Qy       3 VPWFLLSLALGRSPVVLSLERLVGPQDATHCS-------PGLSCRLWDSDILCLPGDIVP 55
           :|   :|      |: |||::   |  |   |       | |     |:  | |||
Db     190 IPSSPMSSVSSYPPLALSLKK---PPTAPDTSASTLPNPPALKKESQDAPGLDLPGAAES 246

Qy      56 APGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEE---------------PE 100
           | |             |||           |   |   | |::                 ||
Db     247 AQG-----------VLR-----------HVKSELGRSGVWKDHWWSTVQPERKSAAPPE 283

Qy     101 D--EEKFGGAADSG-----------------------------------------------V 113
           |   |: ||  : |
Db     284 DAKSEEAGGTKEKGGGQGHGPIAASSRDPHHRRSTGRNGPALSPRTPQSSELSLTGASRS 343

Qy     114 EEPRNASLQAQ--VVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEV 171
           | |:|: | :   | :|  | |                 ||  :  : :|  :  ||
Db     344 ETPQNSPLPSSPIVPMSKPAKP-------------------SVPPLTPEQYEIYMYQEV 383

Qy     172 RIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGP- 230
             |:   ||                :: :|    :   :  |:  |||      ||
Db     384 DTIELTRQVKEK--------------LAKNG----ICQRIFGEKVLGLS------QGSV 418

Qy     231 ------PKPRWHKNLTGPQIITLNHTDLVPCLCIQVW---------------------- 261
                |||  | |          |       | : :|:|
Db     419 SDMLSRPKP-WSK---------LTQKGREPFIRMQLWLNGELGQGVLPVQGQQQGPVLHS 468

Qy     262 ------PLEPDSVRTNICPFRE---DPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEAA 312
                ||:   | :   |       |     :  :  :: ||    |:  ||  | |
Db     469 VTSLQDPLQQGCVSSESTPKTSASCSPAPESPMSSSESVKSLT---ELVQQPCP-PIET- 523

Qy     313 LCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL-LKGHPNLCVQ--VNSSEKL------- 362
           :  | | :|  || |       |     || | ||  | :|  |  | :|
Db     524 ----SKDGKPPEPSDPPAS------DSQPATPLPLSGHSALSIQELVAMSPELDTYGITK 573

Qy     363 QLQECLWADSLGP-LKDDVLLLETRG----------PQDNRSLCALEPSGCTSLPSKAST 411
           :::| |  ::||  |  : :|  |:|          |    ||   ||
Db     574 RVKEVLTDNNLGQRLFGETILGLTQGSVSDLLSRPKPWHKLSLKGREPF---------- 622

Qy     412 RAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLIL 471
                          :||| :|    | :                    :  ::
Db     623 ---------------VRMQLWLND-------PNN------------------VEKLM 639

Qy     472 LLKKDHAKAAARGRAALLLYSADDS--------GFERLVG-------------------- 503
            :|:   ||  : | :    |  ||        | :   |
Db     640 DMKRMEKKAYMKRRHS----SVSDSQPCEPPSVGIDYSQGASPQPQHQLKKPRVVLAPEE 695

Qy     504 --ALASALCQLPL---RVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAV 558
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             ||  |  | |     :   :| ::  |      : |||  | :  :|
Db     696 KEALKRAYQQKPYPSPKTIEELATQLNLKTSTVINWFHNYRSRIRRE------------ 742

Qy     559 ALCSEWLQDGVSG-PGA-HGPHDAFRASLSCVLPDFLQGRAPGSYVGAC--FDRLLHPDA 614
             |  :| |  |  || | |  : |:|          | || |   :|   :    | |
Db     743 -LFIEEIQAGSQGQAGARHSP--SARSS----------GAAPSSEGDSCDGVEAAEGPGA 789

Qy     615 VPALFRTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGT- 673
             |   : |      ||     |  :   ||      :|| |    | :||      | |
Db     790 ADA-EESAPAAAAKSQ----GGPAEAAVAP-----EEREE----APRPAEKRSRRPRGPG 835

Qy     674 PAPGRGVGPGAGPGA 688
           | |||  | |  |||
Db     836 PGPGRRGGGGPAPGA 850


RESULT 11
UL06_HSV11
ID   UL06_HSV11     STANDARD;      PRT;   676 AA.
AC   P10190;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Virion protein UL6.
GN   UL6.
OS   Herpes simplex virus (type 1 / strain 17).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88274327; PubMed=2839594;
RA   McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA   McNab D., Perry L.J., Scott J.E., Taylor P.;
RT   "The complete DNA sequence of the long unique region in the genome of
RT   herpes simplex virus type 1.";
RL   J. Gen. Virol. 69:1531-1574(1988).
RN   [2]
RP   SEQUENCE OF 1-80 FROM N.A.
RX   MEDLINE=88091053; PubMed=2826807;
RA   McGeoch D.J., Dalrymple M.A., Dolan A., McNab D., Perry L.J.,
RA   Taylor P., Challberg M.D.;
RT   "Structures of herpes simplex virus type 1 genes required for
RT   replication of virus DNA.";
RL   J. Virol. 62:444-453(1988).
CC   -!- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA
CC       PACKAGING.
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,
CC       EHV-1 56, EBV BBRF1, HCMV UL104, AND VZV 54.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10879; BAA01652.1; -.
DR   EMBL; X14112; CAA32342.1; -.
DR   EMBL; M19119; AAA45818.2; -.
DR   PIR; F28133; WMBEX6.
DR   InterPro; IPR002660; Herpes_UL6.
DR   Pfam; PF01763; Herpes_UL6; 1.
DR   ProDom; PD003210; Herpes_UL6; 1.
SQ   SEQUENCE   676 AA;  74091 MW;  8CF9D73C6313FAE9 CRC64;

  Query Match             2.8%;  Score 103.5;  DB 1;  Length 676;
  Best Local Similarity   22.5%;  Pred. No. 1.8;
  Matches  102;  Conservative   46;  Mismatches  153;  Indels  153;  Gaps   24;

Qy     295 TLQSWLLDAPCSLPAEAALCWRAPGGD------------PCQPLVPPL--SWENVTVDK 339
           ||:: |||    | |    |: ||||              |  ||| |    |
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Db    130 TLRTTLLDFAHGLVA----CF-APGGPSGPSSFPKYIDWLTCLGLVPILRKRQEGGVTQG 184

Qy    340 VLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEP 399

Db    185 LRAF--LKQHP-----------LTRQLATVAEA----------AERAGPGFFELALAFD- 220

Qy    400 SGCTSLPSKASTRAA-----------RLGEYLLQDL---QSGQCLQLWDDDLGALW---- 441

Db    221 ----------STRVADYDRVYIYYNHRRGDWLVRDPISGQRGECLVLWP----PLWTGDR 266

Qy    442 --------------AC-PMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGR 485

Db    267 LVFDSPVQRLFPEIVACHSLREHAH--------VCRLRNTASVKVLLGRKSDSERGVAGA 318

Qy    486 AALL--LYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTL 543

Db    319 ARVVNKVLGEDD---ETKAGSAASRL----VRLIINMKGMRH------VGDINDTVRSYL 365

Qy    544 QEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVG 603

Db    366 DEAG--------GHL----------IDAPAVDG----------TLPGF--GKGGNSRGS 394

Qy    604 ACFDRLLHPDAVPALFRTVPVFTLPSQLPDFL----GALQQPRAPRSG---RLQERAEQV 656

Db    395 AGQDQGGRAPQLRQAFRTAVVNNINGVLEGYINNLFGTIERLRETNAGLATQLQERDREL 454

Qy    657 SRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGD 690

Db    455 RRATAGALERQQRAADLAAESVTGGCGSRPAGAD 488
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RESULT 12
W70T_MOUSE
ID   W70T_MOUSE     STANDARD;      PRT;   922 AA.
AC   Q9D2V7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   70 kDa WD-repeat tumor rejection antigen homolog.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
CC   -!- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AK018739; BAB31380.1; -.
DR   MGD; MGI:1926135; 0610011B16Rik.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 6.
DR   PRINTS; PR00320; GPROTEINBRPT.
DR   ProDom; PD000018; WD40; 2.
DR   SMART; SM00320; WD40; 6.
DR   PROSITE; PS00678; WD_REPEATS_1; 1.
DR   PROSITE; PS50082; WD_REPEATS_2; 4.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW   Repeat; WD repeat.
FT   REPEAT       75    115       WD 1.
FT   REPEAT      124    163       WD 2.
FT   REPEAT      166    205       WD 3.
FT   REPEAT      209    253       WD 4.
FT   REPEAT      539    581       WD 5.
FT   REPEAT      589    629       WD 6.
FT   REPEAT      632    671       WD 7.
FT   REPEAT      725    765       WD 8.
SQ   SEQUENCE   922 AA;  100860 MW;  C8E4BC1EE9CFE242 CRC64;
```

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  Query Match             2.7%;  Score 102;  DB 1;  Length 922;
  Best Local Similarity   21.1%;  Pred. No. 3.6;
  Matches  146;  Conservative   65;  Mismatches  227;  Indels  254;  Gaps   38;

Qy    130 QAYPTARCVLL-EVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT--QPRYEKELN 186

Db    112 EALPSVPGVVLGPEELPVEVLQFHPTVDGVLV----STAGKTVKVWDVAKQQPLTELEA- 166

Qy    187 HTQQLPALPWLNVSADGDNVHLVL------------------NVSEEQHFGLSLYW--- 224

Db    167 HKDLVQSAVW---SRDGAIVGTACKDKQLRIFDPRARTQASQSTQAHENNRDIRLAWTGI 223

Qy    225 ---------NQVQGPPKPRWHKNLTGPQI--ITLNHT--DLVPCL-------------- 256

Db    224 QEHLVSTGFNQMREREAKLWDTRLFSSALASVTLDTSPGPLIPLLDPDSGLLVLAGKGEN 283

Qy    257 ---CIQVWPLEPDSVRTNICPFRE-------DPRAHQNLWQAARLRLLTLQSWLL----- 301

Db    284 QLYCYEVTPQQPALSPVTQCILENVLRGAALVPRRALAVMSCEVLQVLQLSDTAIIPISH 343

Qy    302 --------------DAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLL 346

Db    344 HVPRKAVEFHEDLFPDTAGSMPASDAHMWWA--GD-----------NQQVQKVSLNPAR 389

Qy    347 KGHPNLCVQVNSSEKLQLQECLWAD---SLGPLKDDVLLLE--------TRGPQDNRSLC 395

Db    390 RPHP---------------CFTSSLVPTMEPAPDMVQPAEMPRADTDLSEGFSSPSSL- 432

Qy    396 ALEPSGCTSL-PSKASTR--AARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKR 452

Db    433 -MSPSTPSSLGPSLSSTSGIGTSPSQRSLQSLLGPSC----------------KFRHTQ 474

Qy    453 WALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFERLVGALASALCQL 512

Db    475 GS----------------LLHRDSHITNLKG--LNLTTPGESDGF----------CAN 504

Qy    513 PLRVAVDLWSRRELSAQGPVAWFHAQR--------RQTLQEGGVVVLL----FSPGAVAL 560

Db    505 RLRVAVPL-----LSSGGEVAVLELQKPGRLPDTALPTLQNGTAVMDLVWDPFDPHRLAV 559

Qy    561 CSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQG--RAPGSYVGACFDRL----LHPDA 614

Db    560 AGE---------------DA-RIRLWRVPPGGLENVLTTPETVLTGHTEKIYSLRFHPLA 603

Qy    615 VPALFR-----TVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQV-SRALQP------ 662

Db    604 ADVLASSSYDLTVRIWDL------------QTGAERL-KLQGHQDQIFSLAWSPDGKQLA 650
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Qy     663 --ALDSY---FHPPGTPAP-GRGVGPGAGPGA 688
             |  :   : |  :| |   | ||  | ||
Db     651 TVCKDGHVRVYEPRSSPLPLQEGPGPEGGRGA 682


RESULT 13
ATC7_YEAST
ID   ATC7_YEAST      STANDARD;      PRT;  1151 AA.
AC   P40527;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Potential phospholipid-transporting ATPase 4 (EC 3.6.3.1).
GN   NEO1 OR YIL048W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RA   Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA   Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA   Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA   Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA   Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA   Walsh S.V., Whitehead S.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS
CC       OF ATP COUPLED WITH THE TRANSPORT OF PHOSPHOLIPIDS (POTENTIAL).
CC       LEADS TO NEOMYCIN-RESISTANCE WHEN OVEREXPRESSED.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC       (E1-E2 ATPASES). SUBFAMILY IV.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z38060; CAA86174.1; -.
DR   PIR; S48431; S48431.
DR   SGD; S0001310; NEO1.
DR   InterPro; IPR001757; ATPase_E1-E2.
DR   InterPro; IPR001454; Hlgnase/hydrlase.
DR   Pfam; PF00122; E1-E2_ATPase; 1.
DR   Pfam; PF00702; Hydrolase; 1.
DR   PROSITE; PS00154; ATPASE_E1_E2; 1.
KW   Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.
FT   TRANSMEM    185    205       POTENTIAL.
FT   TRANSMEM    210    230       POTENTIAL.
FT   TRANSMEM    368    388       POTENTIAL.
FT   TRANSMEM    417    437       POTENTIAL.
FT   TRANSMEM    439    459       POTENTIAL.
FT   TRANSMEM    948    968       POTENTIAL.
FT   TRANSMEM    971    991       POTENTIAL.
FT   TRANSMEM   1021   1041       POTENTIAL.
FT   TRANSMEM   1053   1073       POTENTIAL.
FT   TRANSMEM   1079   1099       POTENTIAL.
FT   TRANSMEM   1110   1130       POTENTIAL.
FT   MOD_RES     503    503       PHOSPHORYLATION (PROBABLE).
SQ   SEQUENCE   1151 AA;  130217 MW;  DC7225CC9577DBE6 CRC64;

  Query Match             2.7%;  Score 101.5;  DB 1;  Length 1151;
  Best Local Similarity   21.1%;  Pred. No. 5.3;
  Matches   64;  Conservative   49;  Mismatches  112;  Indels   79;  Gaps   15;

Qy     102 EEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYD 161
           |:|      | :|  ||| ::   :|:     ||||    | : | |:  || | ::
Db     749 EDKLQKDVKSSIELLRNAGIKIW-MLTGDKVETARC----VSISAKLISRGQYVHTIT-- 801

Qy     162 CFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSA----DGDNVHLVLNVSEEQH 217
                       |:|  |   |  : |     :| :|    ||::: : |   |::
Db     802 ------------KVTRP--EGAFNQLEYLK----INRNACLLIDGESLGMFLKHYEQEF 842

Qy     218 FGLSLYWNQV---QGPPKPRWH-----KNLTGPQIITL----NHTDLVPCLCIQVW---- 261
           | : ::   |   :  |: :       : :|| ::  :    |   :: |  : |
Db     843 FDVVVHLPTVIACRCTPQQKADVALVIRKMTGKRVCCIGDGGNDVSMIQCADVGVGIVGK 902

Qy     262 -----PLEPDSVRTNICPFREDPRAHQNLW-------QAARLRLLTLQSWLLDAPCSLPA 309
                |  |   |  |   |       ||       :::|:|    :   |:: |  |
Db     903 EGKQASLAADFSITQFCHLTE-----LLLWHGRNSYKRSAKLAQFVMHRGLIIAICQ--A 955

Qy     310 EAALC----------WRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNS 358
             ::|           |  |  |  : |  |   :|:|  :|  | | :| |  ::
Db     956 VYSICSLFEPIALYQGWLMVGYATCYTMAPVFS---LTLDHDIEESLTKIYPELYKELTE 1012

Qy     359 SEKL 362
             :|
Db    1013 GKSL 1016


RESULT 14
UL06_HSVEB
ID   UL06_HSVEB      STANDARD;      PRT;   753 AA.
AC   P28944;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Virion gene 56 protein.
GN   56.
OS   Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Varicellovirus.
OX   NCBI_TaxID=31520;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92295566; PubMed=1318606;
RA   Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT   "The DNA sequence of equine herpesvirus-1.";
RL   Virology 189:304-316(1992).
CC   -!- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA
CC       PACKAGING.
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6,
CC       EHV-1 56, EBV BBRF1, HCMV UL104, AND VZV 54.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M86664; AAB02491.1; -.
DR   PIR; B36801; WZBEE8.
DR   InterPro; IPR002660; Herpes_UL6.
DR   Pfam; PF01763; Herpes_UL6; 1.
DR   ProDom; PD003210; Herpes_UL6; 1.
SQ   SEQUENCE   753 AA;  83992 MW;  C5E118F78BBED203 CRC64;

  Query Match             2.7%;  Score 100.5;  DB 1;  Length 753;
  Best Local Similarity   22.9%;  Pred. No. 3.7;
  Matches   99;  Conservative   46;  Mismatches  190;  Indels   97;  Gaps   20;

Qy     295 TLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV 354
           |||  |||   |: |    |: |    |          : |  :    ::    ||  |   |
Db     156 TLQMSLLDFVRSITA----CFSASEPDGTASFAKYIDW--IACLGLIPLQRLKRAPGATV 209

Qy     355 QVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSL----------------CALE 398
                     ||      |  ||  ||:    | | |                   :|
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Db    210 HPK----------LWR----KLPTDVPSLES--CVDERDLAGKLYVANSLLREGLEAVVE 253

Qy    399 PSGCT-SLPSKASTRAARLGEYLLQDL--------QSGQCLQLWD---DDLGALWACPMD 446
          : || |:      |       |  :::         : |:|| ||     |   |:  |:
Db    254 LARCTASVAIMDYDRVNIFYHYTRREVVAIDSTTGKRGECLVLWQPIWKDGSVLFDSPLQ 313

Qy    447 KY------IHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSGFER 500
          :        |       |  ||    : :::  ||| |:    | |:  :      | |
Db    314 RICGEVCNCHALREHAKLCQLLNTVPVKILVGRKKDEAQGP--GWASKAVDKLMGEGEEL 371

Qy    501 LVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVAL 560
          : || |    ::: |:: | | :         :     |    |  |    ||
Db    372 HSSSAASRL----VKLIVNMKSMRHIGDITETVRSYLNETSTNLLSGAQVDTSLPG---- 423

Qy    561 CSEWLQDGVSGPGAHGP-HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALF 619
             : | | :  | : |  :||| |:   :   |:|     ||               ||
Db    424 ---FGQSGKTKQGGNMPVQEAFRTSVINGINGMLEG-----YVN------------NLF 462

Qy    620 RTVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPA--PG 677
          :|:      :      | | | |  |   :    ||: |  | | |    |  : |  ||
Db    463 KTIEDLRTGNS-----GLLDQLR-DRESEITHLREQLLRVSQAAADGSTQPGASSAALPG 516

Qy    678 RGVGPGAGPGAG 689
          |   ||| | |
Db    517 SGAKSGAG-GLG 527


RESULT 15
CLR3_HUMAN
ID   CLR3_HUMAN     STANDARD;      PRT;  3312 AA.
AC   Q9NYQ7; O75092;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Cadherin EGF LAG seven-pass G-type receptor 3 precursor (Flamingo
DE   homolog 1) (hFmil) (Multiple epidermal growth factor-like domains 2)
DE   (Epidermal growth factor-like 1).
GN   CELSR3 OR CDHF11 OR FMI1 OR EGFL1 OR MEGF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20202599; PubMed=10716726;
RA   Wu Q., Maniatis T.;
RT   "Large exons encoding multiple ectodomains are a characteristic
RT   feature of protocadherin genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
RN   [2]
RP   SEQUENCE OF 1954-3312 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98360089; PubMed=9693030;
RA   Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT   "Identification of high-molecular-weight proteins with multiple
RT   EGF-like motifs by motif-trap screening.";
RL   Genomics 51:27-34(1998).
CC   -!- FUNCTION: Receptor that may have an important role in cell/cell
CC       signaling during nervous system formation.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC   -!- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
CC   -!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF231023; AAF61929.1; -.
DR   EMBL; AB011536; BAA32464.1; -.
DR   HSSP; P00740; 1EDM.
DR   Genew; HGNC:3230; CELSR3.
DR   MIM; 604264; -.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR002126; Cadherin.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR000832; GPCR_secretin.
DR   InterPro; IPR001879; hormn_receptor.
DR   InterPro; IPR002049; Laminin_EGF.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR000203; PKD_cys_rich.
DR   Pfam; PF00002; 7tm_2; 1.
DR   Pfam; PF00028; cadherin; 9.
DR   Pfam; PF00008; EGF; 6.
DR   Pfam; PF01825; GPS; 1.
DR   Pfam; PF02793; HRM; 1.
DR   Pfam; PF00054; laminin_G; 2.
DR   PRINTS; PR00205; CADHERIN.
DR   PRINTS; PR00011; EGFLAMININ.
DR   PRINTS; PR00249; GPCRSECRETIN.
DR   SMART; SM00112; CA; 8.
DR   SMART; SM00180; EGF_Lam; 1.
DR   SMART; SM00001; EGF_like; 6.
DR   SMART; SM00303; GPS; 1.
DR   SMART; SM00008; HormR; 1.
DR   SMART; SM00282; LamG; 2.
DR   PROSITE; PS00010; ASX_HYDROXYL; 1.
DR   PROSITE; PS00232; CADHERIN_1; 7.
DR   PROSITE; PS50268; CADHERIN_2; 8.
DR   PROSITE; PS00022; EGF_1; 6.
DR   PROSITE; PS01186; EGF_2; 4.
DR   PROSITE; PS50221; GPS; 1.
DR   PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
DR   PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR   PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR   PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
DR   PROSITE; PS50025; LAM_G_DOMAIN; 2.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
KW   Developmental protein; Hydroxylation; Signal.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33   3312       CADHERIN EGF LAG SEVEN-PASS G-TYPE
FT                                RECEPTOR 3.
FT   DOMAIN       33   2540       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   2541   2561       1 (POTENTIAL).
FT   DOMAIN     2562   2572       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   2573   2593       2 (POTENTIAL).
FT   DOMAIN     2594   2601       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   2602   2622       3 (POTENTIAL).
FT   DOMAIN     2623   2643       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   2644   2664       4 (POTENTIAL).
FT   DOMAIN     2665   2681       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   2682   2702       5 (POTENTIAL).
FT   DOMAIN     2703   2725       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   2726   2746       6 (POTENTIAL).
FT   DOMAIN     2747   2753       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   2754   2774       7 (POTENTIAL).
FT   DOMAIN     2775   3312       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      326    433       CADHERIN 1.
FT   DOMAIN      434    545       CADHERIN 2.
FT   DOMAIN      546    651       CADHERIN 3.
FT   DOMAIN      652    756       CADHERIN 4.
FT   DOMAIN      757    858       CADHERIN 5.
FT   DOMAIN      859    961       CADHERIN 6.
FT   DOMAIN      962   1067       CADHERIN 7.
FT   DOMAIN     1068   1169       CADHERIN 8.
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FT   DOMAIN     1170   1265       CADHERIN 9.
FT   DOMAIN     1375   1433       EGF-LIKE 1, CALCIUM-BINDING.
FT   DOMAIN     1435   1471       EGF-LIKE 2, CALCIUM-BINDING.
FT   DOMAIN     1475   1514       EGF-LIKE 3, CALCIUM-BINDING.
FT   DOMAIN     1515   1719       LAMININ G-LIKE 1.
FT   DOMAIN     1722   1758       EGF-LIKE 4, CALCIUM-BINDING.
FT   DOMAIN     1764   1944       LAMININ G-LIKE 2.
FT   DOMAIN     1946   1982       EGF-LIKE 5, CALCIUM-BINDING.
FT   DOMAIN     1983   2020       EGF-LIKE 6, CALCIUM-BINDING.
FT   DOMAIN     2021   2053       EGF-LIKE 7, CALCIUM-BINDING.
FT   DOMAIN     2055   2090       EGF-LIKE 8, CALCIUM-BINDING.
FT   DOMAIN     2096   2131       LAMININ EGF-LIKE.
FT   DOMAIN     2477   2529       GPS.
FT   DISULFID   1379   1390       BY SIMILARITY.
FT   DISULFID   1384   1421       BY SIMILARITY.
FT   DISULFID   1423   1432       BY SIMILARITY.
FT   DISULFID   1439   1450       BY SIMILARITY.
FT   DISULFID   1444   1459       BY SIMILARITY.
FT   DISULFID   1461   1470       BY SIMILARITY.
FT   DISULFID   1479   1490       BY SIMILARITY.
FT   DISULFID   1484   1500       BY SIMILARITY.
FT   DISULFID   1502   1513       BY SIMILARITY.
FT   DISULFID   1726   1737       BY SIMILARITY.
FT   DISULFID   1731   1746       BY SIMILARITY.
FT   DISULFID   1748   1757       BY SIMILARITY.
FT   DISULFID   1950   1961       BY SIMILARITY.
FT   DISULFID   1955   1970       BY SIMILARITY.
FT   DISULFID   1972   1981       BY SIMILARITY.
FT   DISULFID   1985   1996       BY SIMILARITY.
FT   DISULFID   1990   2008       BY SIMILARITY.
FT   DISULFID   2010   2019       BY SIMILARITY.
FT   DISULFID   2019   2037       BY SIMILARITY.
FT   DISULFID   2027   2040       BY SIMILARITY.
FT   DISULFID   2042   2052       BY SIMILARITY.
FT   DISULFID   2059   2074       BY SIMILARITY.
FT   DISULFID   2061   2077       BY SIMILARITY.
FT   DISULFID   2079   2089       BY SIMILARITY.
FT   MOD_RES    1963   1963       HYDROXYLATION (POTENTIAL).
FT   CARBOHYD    632    632       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    847    847       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1182   1182       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1222   1222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1317   1317       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1327   1327       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1649   1649       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1713   1713       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   1770   1770       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2053   2053       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2177   2177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2196   2196       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2386   2386       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2474   2474       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   2506   2506       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   2158   2158       G -> GLRGAG (IN REF. 2).
SQ   SEQUENCE   3312 AA;  358251 MW;  BEC208703651A4A5 CRC64;

  Query Match             2.7%;  Score 100.5;  DB 1;  Length 3312;
  Best Local Similarity   19.8%;  Pred. No. 25;
  Matches  190;  Conservative   78;  Mismatches  301;  Indels  393;  Gaps   47;

Qy      26 GPQDATHCSPGLSCR-LWDS-DILCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDCDLC 83
           ||     | |   || || :    | ||          |  :   |:  || :  |
Db    1953 GP-----CPPHADCRDLWQTFSCTCQPG--------YYGPGCVDACLLNPCQNQGSCR-- 1997

Qy      84 LRVAVHL--AVHG------------HWEEPEDEEKFGGAADSGVEEPRNASLQ------- 122
             ||  | ||              | |   |::   |   |    | |  :
Db    1998 -----HLPGAPHGYTCDCVGGYFGHHCEHRMDQQCPRGWWGSPTCGPCNCDVHKGFDPNC 2052

Qy     123 ------------------AQVVLSFQAYP---TAR-CVLLEVQVPAALVQFGQSVGS--- 157
                           :   |    ||   |:| |     | |      |:   |
Db    2053 NKTNGQCHCKEFHYRPRGSDSCLPCDCYPVGSTSRSCAPHSGQCPCRPGALGRQCNSCDS 2112

Qy     158 -----------VVYD-----------------------CFEAALGSEVRIWSYTQPRYE 182
                      |:||                      |   |||: ||:    |   |
Db    2113 PFAEVTASGCRVLYDACPKSLRSGVWWPQTKFGVLATVPCPRGALGAAVRLCDEAQGWLE 2172

Qy     183 KEL-NHTQQLPALPWLNVSADG-------------------------DN--------- 205
           :| | |   ||   |:  ||                          |:
Db    2173 PDLFNCTS--PAFRELSLLLDGLELNKTALDTMEAKKLAQRLREVTGHTDHYFSQDVRVT 2230

Qy     206 ----VHLV----------LNVSEEQHFGLSLYWN-------------QVQGPPKPRWHKN 238
                ||:          |  ::: ||  :| |                 |   |
Db    2231 ARLLAHLLAFESHQQGFGLTATQDAHFNENLLWAGSALLAPETGDLWAALGQRAPGGSPG 2290

Qy     239 LTG--------------PQIITLNHTDLV-PCLCIQVWPLE-PDSVRTNICPFREDPRA 281
             |                ::  ||   || | : : :  :| | | |      |  ||
Db    2291 SAGLVRHLEEYAATLARNMELTYLNPMGLVTPNIMLSIDRMEHPSSPR----GARRYPRY 2346

Qy     282 HQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVL 341
           | ||::          :|       ||::      :|   | : |    | || |   |:
Db    2347 HSNLFRGQ-------DAWDPHTHVLLPSQ------SPRPSPSEVLPTSSSIENSTTSSVV 2393

Qy     342 EFPL-LKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRG---PQD------- 390
             |   :  | : : :          |  :|| |       | ||   ||:
Db    2394 PPPAPPEPEPGISIII----------LLVYRTLGGLLPAQFQAERRGARLPQNPVMNSPV 2443

Qy     391 ----------------------------NRS--LCA-LEPSG-----------CTSL 405
                                        |||  :|   :| |           |  :
Db    2444 VSVAVFHGRNFLRGILESPISLEFRLLQTANRSKAICVQWDPPGLAEQHGVWTARDCELV 2503

Qy     406 ---PSKASTRAARLGEY-LLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACL 461
           | |  | :| | : :| |     : |   : ||  |       : |   |:   | :
Db    2504 HRNGSHARCRCSRTGTFGVLMDASPRERL---EGDLELLAV-----FTHVVVAVSVAALV 2555

Qy     462 LFAAALSLILLLKKD----HAK-AAARGRAALL-------------------------- 489
           | || |  :  || :    ||  ||| | | ||
Db    2556 LTAAILLSLRSLKSNVRGIHANVAAALGVAELLFLLGIHRTHNQLVCTAVAILLHYFFLS 2615

Qy     490 -----------LYSAD------DSGFERLVGALASALCQLPLRVAVDL----------W 521
                      ||          | |  |   ||   :  : | :|| |          |
Db    2616 TFAWLFVQGLHLYRMQVEPRNVDRGAMRFYHALGWGVPAVLLGLAVGLDPEGYGNPDFCW 2675

Qy     522 SRRELSAQGPVAWFHA-------------------------QRRQ------TLQEGGVVV 550
             :|   |: |  |                           ||        ||:   :::
Db    2676 ----ISVHEPLIWSFAGPVVLVIVMNGTMFLLAARTSCSTGQREAKKTSALTLRSSFLLL 2731

Qy     551 LLFSP----GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACF 606
           || |     | :|:    |        |  |         | ||    |   |  ::: ||
Db    2732 LLVSASWLFGLLAVNHSILAFHYLHAGLCGLQGLAVLLLFCV----LNADARAAWMPACL 2787

Qy     607 DRLLHPDAV-------PALFRTVPVFTLPSQLPDFLGA--LQQPRAPRSGRLQERAEQVS 657
             |   |:         |  :    :|     :   |||  :    : |||| |::  |
Db    2788 GRKAAPEEARPAPGLGPGAYNNTALFEESGLIRITLGASTVSSVSSARSGRTQDQDSQRG 2847

Qy     658 RA 659
           |:
Db    2848 RS 2849


Search completed: February 24, 2003, 09:21:56
Job time : 27 secs
```

GenCore version 5.1.3


OM protein - protein search, using sw model

Run on: February 24, 2003, 09:21:27 ; Search time 41 Seconds
(without alignments)
3477.673 Million cell updates/sec

Title: US-09-608-918-2
Perfect score: 3716
Sequence: 1 MPVPWFLLSLALGRSPVVLS.....TPAPGRGVGPGAGPGAGDGT 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2598 | 69.9 | 538 | 4 | Q9BR97 | Q9br97 homo sapien |
| 2 | 1812.5 | 48.8 | 567 | 11 | Q99J43 | Q99j43 mus musculu |
| 3 | 215 | 5.8 | 311 | 11 | Q8R335 | Q8r335 mus musculu |
| 4 | 131.5 | 3.5 | 4340 | 2 | O30764 | O30764 streptomyce |
| 5 | 131 | 3.5 | 482 | 4 | Q8TEC2 | Q8tec2 homo sapien |
| 6 | 130.5 | 3.5 | 1366 | 16 | Q9Z529 | Q9z529 streptomyce |
| 7 | 116.5 | 3.1 | 1665 | 11 | Q8VII1 | Q8vii1 mus musculu |
| 8 | 116 | 3.1 | 1021 | 4 | Q96M86 | Q96m86 homo sapien |
| 9 | 115.5 | 3.1 | 745 | 16 | Q8XED7 | Q8xed7 escherichia |
| 10 | 114.5 | 3.1 | 745 | 2 | Q9EYF6 | Q9eyf6 escherichia |
| 11 | 114.5 | 3.1 | 1193 | 16 | Q9HZE5 | Q9hze5 pseudomonas |
| 12 | 112.5 | 3.0 | 657 | 4 | Q96DW2 | Q96dw2 homo sapien |
| 13 | 112.5 | 3.0 | 744 | 4 | Q96F55 | Q96f55 homo sapien |
| 14 | 111.5 | 3.0 | 405 | 17 | Q8TZU1 | Q8tzu1 pyrococcus |
| 15 | 111.5 | 3.0 | 478 | 16 | Q9RY89 | Q9ry89 deinococcus |
| 16 | 111 | 3.0 | 1279 | 12 | Q66031 | Q66031 cercopithec |
| 17 | 110 | 3.0 | 757 | 6 | Q9N015 | Q9n015 macaca fasc |
| 18 | 109.5 | 2.9 | 620 | 4 | Q9HCN6 | Q9hcn6 homo sapien |
| 19 | 109 | 2.9 | 427 | 2 | Q9S1L6 | Q9s116 streptovert |
| 20 | 109 | 2.9 | 603 | 12 | P89140 | P89140 pseudorabie |
| 21 | 109 | 2.9 | 604 | 12 | Q9YVB7 | Q9yvb7 pseudorabie |
| 22 | 109 | 2.9 | 1343 | 12 | Q06635 | Q06635 bovine herp |
| 23 | 108.5 | 2.9 | 1072 | 4 | Q96EP0 | Q96ep0 homo sapien |
| 24 | 108 | 2.9 | 361 | 2 | O86440 | O86440 pseudomonas |
| 25 | 108 | 2.9 | 2629 | 11 | P97499 | P97499 mus musculu |
| 26 | 108 | 2.9 | 10917 | 2 | Q93NW6 | Q93nw6 streptomyce |
| 27 | 107 | 2.9 | 719 | 16 | O69992 | O69992 streptomyce |
| 28 | 107 | 2.9 | 1001 | 16 | Q9KZM8 | Q9kzm8 streptomyce |
| 29 | 107 | 2.9 | 1118 | 4 | Q15426 | Q15426 homo sapien |
| 30 | 107 | 2.9 | 4928 | 2 | Q9ALM3 | Q9alm3 saccharopol |
| 31 | 106.5 | 2.9 | 679 | 16 | Q9F2P6 | Q9f2p6 streptomyce |
| 32 | 106 | 2.9 | 1211 | 11 | Q9R0L3 | Q9r0l3 rattus norv |
| 33 | 106 | 2.9 | 1235 | 11 | Q9R0L5 | Q9r015 rattus norv |
| 34 | 106 | 2.9 | 1273 | 11 | Q9R0L4 | Q9r014 rattus norv |
| 35 | 106 | 2.9 | 1531 | 5 | Q9W0P8 | Q9w0p8 drosophila |
| 36 | 106 | 2.9 | 9510 | 2 | Q93NX9 | Q93nx9 streptomyce |
| 37 | 105.5 | 2.8 | 1354 | 11 | Q9EPW8 | Q9epw8 mus musculu |
| 38 | 105.5 | 2.8 | 1542 | 4 | O15035 | O15035 homo sapien |
| 39 | 105 | 2.8 | 1766 | 12 | Q9J599 | Q9j599 fowlpox vir |
| 40 | 104.5 | 2.8 | 277 | 16 | O53500 | O53500 mycobacteri |
| 41 | 104 | 2.8 | 1256 | 11 | Q99M76 | Q99m76 rattus norv |
| 42 | 104 | 2.8 | 1487 | 5 | O15843 | O15843 leishmania |
| 43 | 103.5 | 2.8 | 828 | 16 | Q8ZBL4 | Q8zbl4 yersinia pe |
| 44 | 103.5 | 2.8 | 2055 | 4 | O75055 | O75055 homo sapien |
| 45 | 103 | 2.8 | 384 | 4 | Q8TDX1 | Q8tdx1 homo sapien |

ALIGNMENTS

RESULT 1
Q9BR97
ID Q9BR97 PRELIMINARY; PRT; 538 AA.
AC Q9BR97;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 59.1 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC006411; AAH06411.1; -.
KW Hypothetical protein.
SQ SEQUENCE 538 AA; 59127 MW; 65E6344DA6A5AFD2 CRC64;

Query Match 69.9%; Score 2598; DB 4; Length 538;
Best Local Similarity 99.4%; Pred. No. 6.1e-207;
Matches 480; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60

Qy      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120

Qy     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180

Qy     181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    181 YEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLT 240

Qy    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL 300

Qy    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE 360

Qy    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 KLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYL 420

Qy    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKG 480

Qy    481 AAR 483
             |
Db    481 WLR 483


RESULT 2
Q99J43
ID   Q99J43      PRELIMINARY;      PRT;   567 AA.
AC   Q99J43;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 62.8 kDa protein.
GN   IL17RL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC004759; AAH04759.1; -.
DR   MGD; MGI:2159336; Il17rl.
KW   Hypothetical protein.
SQ   SEQUENCE   567 AA;  62798 MW;  C1AAAB79E2006B1D CRC64;

  Query Match             48.8%;  Score 1812.5;  DB 11;  Length 567;
  Best Local Similarity   62.9%;  Pred. No. 8.8e-142;
  Matches  357;  Conservative   50;  Mismatches  130;  Indels   31;  Gaps    7;

Qy      1 MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPV 60
          ||| |||||||||||:|||:|||||: |||   || |||| ||| |:||||| :  |||||
Db      1 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCLPGSLQSAPGPV 60

Qy     61 LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNAS 120
          | || |||||||||  ::||| ||:|| |||||||||  |||:     | :|| ::| ||||
Db     61 LVPTRLQTELVLRCPQKTDCALCVRVVVHLAVHGHWAEPEE----AGKSDSELQESRNAS 116

Qy    121 LQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR 180
          ||||||||||||| ||| |||||||| ||| |||||| |:|||||:||:||:|||||:||
Db    117 LQAQVVLSFQAYPIARCALLEVQVPADLVQPGQSVGSAVFDCFEASLGAEVQIWSYTKPR 176

Qy    181 YEKELNHTQQLP---------------ALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWN 225
          |:|||| |||||                |||||| ||||| | |:||||| |   ||
Db    177 YQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVSTDGDNVLLTLDVSEEQDFSFLLYLR 236

Qy    226 QVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL 285
            |    |  |:|||||| |||||||||||||||| ||||| |   ||||||| ||:||
Db    237 PVPDALKSLWYKNLTGPQNITLNHTDLVPCLCIQVWSLEPDSERVEFCPFREDPGAHRNL 296

Qy    286 WQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPL 345
          |  ||||:|:   | ||||| || :  |||:||  |||||||:  :| ||::  :| |
Db    297 WHIARLRVLSPGVWQLDAPCCLPGKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQL 356

Qy    346 LKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSL 405
          : |||||||||:: ||:||| |||||||| |||:||:| :   :| |:||||||||| |
Db    357 VAGHPNLCVQVSTWEKVQLQACLWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPL 416

Qy    406 PSKASTRAARLGEYLLQDLQSGQCLQLW-DDDLGALWACPMDKYIHKRWALVWLACLLFA 464
          || |||||||||| |||| :| ||:||| ||::|:|||||||||||:|| |||||||| |
Db    417 PSMASTRAARLGEELLQDFRSHQCMQLWNDDNMGSLWACPMDKYIHRRWVLVWLACLLLA 476

Qy    465 AALSLILLLKKDHAKAAARGRAALLLYS------ADDSGFERLVGALASALCQLPLRVAV 518
          |||   ||||||    :  | ||    |      |  ||     |     ||  | | |
Db    477 AALFFFLLLKKDRMTPSPPGSAACYPISCKAGRPAATSG-STSTGCCTQTLC--PPRSAS 533

Qy    519 DLWSRRELSAQGPVAWFHAQRRQTLQEG 546
             |    | :  ::| | :    |  |
Db    534 PRSSPCPRSCR--LSWMHCREAAPLPRG 559


RESULT 3
Q8R335
ID   Q8R335      PRELIMINARY;      PRT;   311 AA.
AC   Q8R335;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 34.1 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026737; AAH26737.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   311 AA;  34102 MW;  00E706D6617CFF15 CRC64;

  Query Match             5.8%;  Score 215;  DB 11;  Length 311;
  Best Local Similarity   29.0%;  Pred. No. 1.1e-09;
  Matches   81;  Conservative   33;  Mismatches  117;  Indels   48;  Gaps   10;

Qy    418 EYLLQDLQSGQCLQLWDDDLGALW---ACPMDKYIHKRWALVWLACLLFAAALSLIL-LL 473
          : ::  |:   |: :|  |:   |    ||     |:   |: || |   | : ::| ||
Db     53 DLIIPFLRQENCILVWRSDVQFAWKHVLCP--DVSHRHLGLLILALLALTALVGVVLVLL 110

Qy    474 KKDHAKAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVA--------VDLWSRRE 525
          :     : | |  |||::||     |||||||       || |        ||||
Db    111 GRRLLPGSGRTRPVLLLHAADSEAQRRLVGALAEL-----LRTALGGGRDVIVDLWEGTH 165

Qy    526 LSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASL 585
          ::  ||: |  | | :  :| | |:||::                :||      |   |||
Db    166 VARIGPLPWLWAARERVAREQGTVLLLWN-------------CAGPSTACSGDPQAASL 211

Qy    586 SCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLGALQ-QPRAP 644
            :|       ||   : | | ||     :|   | :| : |   ||  | ||  ||
Db    212 RTLL-----CAAPRPLLLAYFSRLCAKGDIPRPLRALPRYRLLRDLPRLLRALDAQPATL 266

Qy    645 RSG--------RLQERAEQVS-RALQPALDSYFHPPGTP 674
            |          |: | ||     |: | | |     :|
Db    267 ASSWSHLGAKRCLKNRLEQCHLLELEAAKDDYQGSTNSP 305


RESULT 4
O30764
ID   O30764      PRELIMINARY;      PRT;  4340 AA.
AC   O30764;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Polyketide synthase modules 1 and 2.
GN   NIDA1.
OS   Streptomyces caelestis.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=36816;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRRL-2821;
RX   MEDLINE=98053867; PubMed=9393718;
RA   Kakavas S.J., Katz L., Stassi D.;
RT   "Identification and characterization of the niddamycin polyketide
RT   synthase genes from Streptomyces caelestis.";
RL   J. Bacteriol. 179:7515-7522(1997).
CC   -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC       (SDR) FAMILY.
DR   EMBL; AF016585; AAC46024.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR001227; Ac_transferase.
DR   InterPro; IPR002198; ADH_short.
DR   InterPro; IPR004410; FabD.
DR   InterPro; IPR000794; Ketoacyl-synt.
DR   InterPro; IPR003880; Ppantne_attach.
DR   Pfam; PF00698; Acyl_transf; 3.
DR   Pfam; PF00106; adh_short; 2.
DR   Pfam; PF00109; ketoacyl-synt; 3.
DR   Pfam; PF02801; ketoacyl-synt_C; 3.
DR   Pfam; PF00550; pp-binding; 3.
DR   TIGRFAMs; TIGR00128; fabD; 3.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR   PROSITE; PS50075; ACP_DOMAIN; 3.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
KW   Oxidoreductase; Phosphopantetheine; Transferase.
SQ   SEQUENCE   4340 AA;  457589 MW;  D59A734CB5FB795D CRC64;

  Query Match             3.5%;  Score 131.5;  DB 2;  Length 4340;
  Best Local Similarity   21.5%;  Pred. No. 0.3;
  Matches  146;  Conservative   60;  Mismatches  225;  Indels  247;  Gaps   30;

Qy     168 GSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQV 227
           |    :    |  ::: : ||       || ||                |   |   : :
Db    1692 GPRTALEETAQQLHQQGIRHT-------WLKVS---------------HAFHSALMDPM 1728

Qy     228 QG------------PPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLE--------PDS 267
            |            ||      |||| ||   ||      ||   : ::         |:
Db    1729 LGAFRDTLNTLNYQPPTIPLISNLTG-QIADPNH------LCTPDYWIDHARHTVRFADA 1781

Qy     268 VRTNICPFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPA-----------EAALCWR 316
           |:|       | |    |   |   | ||    || | ::|              ||
Db    1782 VQT-----AHDQRTTTYLEIGAHPTLTTLLHHTLDNPTTIPTLHREHPEPETLTTALATL 1836

Qy     317 APGGD----------------PCQPLVPPLSW-ENVTVDKVLEFPLLKGHPNLCVQVNSS 359
             |                  |  |      | | | | :|       | |        :
Db    1837 HTTGHTTTLHTTSPQTHHLDLPTYPFQRDRYWMEPVRVAQV------SGQP-------GA 1883

Qy     360 EKLQLQ---ECLWADSLGPLKDDVLLLETRGPQDNRSLCALE----------------P 399
           ::|: :   |    |   |  :  |||    | |   |  :|                |
Db    1884 DRLRYRVVWEAAPEDHTVPSAERWLLLGGSDPADAGILVGVEEQLVGHGAAVQRLDIPAP 1943

Qy     400 SG------CTSLPSKAST----------RAARLGE--YLLQDL-QSGQCLQLWDDDLGAL 440
           :|      |: || :  :           |: |: |   ||| |  :|    ||    ||:
Db    1944 AGRRLLPSCSELPVRGPSHTGEFCGSRLRSPRVAEAVALLQALGDAGADAPLWIATRGAV 2003

Qy     441 WACPMDKYI---HKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAALLLYSADDSG 497
            |   :       : | |  :| |   |     :: |  | | || || | :|: :| |:
Db    2004 AAQAGEAPSVGGAQLWGLGQVAGLELADRWGGLVDLPADPAPAALRGLARVLVSNAPDN- 2062

Qy     498 FERLVGALASALCQLPLRVAVDLWSRRELSAQG-PVAWFHAQRRQTLQEGGVVVLLFSPG 556
                  |: :| |  :: || : | | ||
Db    2063 ------------QVAIR-ASGVFVRRVVPAPGRPVR---------------------- 2085

Qy     557 AVALCSEWLQDG----VSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRL--- 609
           ::|   |       | || |   | | :|:      | ||   |      | |
Db    2086 -----NDWAPSGTVLITGGTGALGSQVARRLALAGAPHLLLAGRRGNSGAAELVDELTAL 2140

Qy     610 -----------LHPDAVPALFRTVPVF---------------TLPSQLPDFLGALQQPR 642
                      ||: :|  |:|                   |    |: : |: : :
Db    2141 GAEVTVAACDAADRDALVSLLATIPEHRPLTAVLHAAGVLDDGVLDGLTPERIDAVLRAK 2200

Qy     643 APRSGRLQERAEQVS---------------------RALQPALDSYFHPPGTPAPGRGV 680
           |  :  | |    :                     |   |||:  |  |  | |:
Db    2201 ATAARHLDELTADLDLDAFVLFSSIVGVWGNGGQATYAAANAALDALAH--GRRARGQRA 2258

Qy     681 -----GPGAGPG--AGDG 691
                || || |  ||||
Db    2259 TSIAWGPWAGSGMAAGDG 2276


RESULT 5
Q8TEC2
ID   Q8TEC2      PRELIMINARY;      PRT;   482 AA.
AC   Q8TEC2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA FLJ23658 fis, clone COLF3416.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON MUCOSA;
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA   Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK074238; BAB85028.1; -.
SQ   SEQUENCE   482 AA;  54139 MW;  4164B5A73026B385 CRC64;

  Query Match             3.5%;  Score 131;  DB 4;  Length 482;
  Best Local Similarity   31.7%;  Pred. No. 0.018;
  Matches   45;  Conservative   18;  Mismatches   45;  Indels   34;  Gaps    7;

Qy     237 KNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAH-QNLWQAAR----- 290
           | ::|   : | :  |:|||||:   |: |:||   |||:  | |:  : |::
Db     223 KIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYS 282

Qy     291 -----LRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDK-----V 340
                :  |||:       | |  ||||| |      |: |       | |  :     |
Db     283 QHTQMVMALTLR------CPLKLEAALCQRHDWHTLCKDL------PNATARESDGWYV 329

Qy     341 LEFPLLKGHPNLCVQV---NSS 359
           ||   |  || || :    |||
Db     330 LEKVDL--HPQLCFKFSFGNSS 349


RESULT 6
Q9Z529
ID   Q9Z529      PRELIMINARY;      PRT;  1366 AA.
AC   Q9Z529;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative large Pro/Ala/Gly-rich protein.
GN   SCO5710 OR SC9F2.06C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Murphy L., Harris D.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
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RA   Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL035559; CAB37473.1; -.
SQ   SEQUENCE   1366 AA;  141042 MW;  FB954569D87D029B CRC64;

  Query Match             3.5%;  Score 130.5;  DB 16;  Length 1366;
  Best Local Similarity   22.4%;  Pred. No. 0.079;
  Matches  175;  Conservative   57;  Mismatches  238;  Indels  311;  Gaps   42;

Qy      21 LERLVGPQDATHCSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDC 80
           |:  :   || |    |: ||       |||   ||| ||         | |
Db     675 LDGALADPDAGH---PLTIRLLSEVRAALPGP--PAPVPVTRDAVFTAYLDL-------- 721

Qy      81 DLCLRVAVHLAVHGHWEEPEDEEKFGGAA--------DSGVEEPRNASL-QAQVVLSFQA 131
            :|||||  ||         ||    | |          | |    ||   | |  ::
Db     722 -MCLRVATRLA---------DENGLRGTAVRRLAAKVSGQVHEAARRSLGPGQGGLDRES 771

Qy     132 YPT-----------------ARCVLLE-VQVPAAL-----------------VQFGQSVG 156
           : |                  |  || | : ||                    :  |:::
Db     772 FETLFPCGPAPARLGGGTGWAPAVLAEGLFVPTGSGYRFAHEELADWIQGTHLDLGEALR 831

Qy     157 SVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQ 216
           ::|:   :  ||:                  ||: || :|   :   |  |  :| ::  |
Db     832 ALVHR-RDTPLGT----------------HTRTLP-VPHHRI---GSVVEALLLLA-RQ 868

Qy     217 HFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFR 276
           |          | |:          : |   :||  |
Db     869 H----------GVPQ-----------LALTLEELVHAL-----------------D 886

Qy     277 EDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEAAL-------CWRAPGGDPCQPLVPP 329
           || :    | ||||    |   |   | : |    |          ||  | |   :  |
Db     887 RDPHS----WWAARL----LAEALTRVPDATPYTDVLRLLADGIAERAGDGQPTPQVFGP 938

Qy     330 LSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQ 389
           |    |       ||:                :| | :                    ||
Db     939 AFWTAPRVPAATRLDLLR------------RLVLAD-------------------GPP 965

Qy     390 DNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQL-WDDDLGALWACPMDKY 448
               ||      |   | |      |: | :: | | : | ||    | | |
Db     966 H-------EPG-----PRHLDTAAG----LLVADPRTVQPLLVRWFDDERPLPATP---- 1005

Qy     449 IHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAAL------------LLYSADD 495
                                    ||  |   :| |              :|  :
Db    1006 ----------------------------HATVATAAQALLHTHRHRGLDGLTEVLVDSTH 1037

Qy     496 SGFERLVGALA----SALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRR---------QT 542
              : |:  ||    ||||:     ||: |:| |  |:   |  |  |           :|
Db    1038 RRADELLAVLAEEEPSALCR-----AVERWARDERPARHRAAVTHGLRTAPHARSGADRT 1092

Qy     543 LQEGGVVVLLFSP-------GAVALCSEWLQDGVSGPGAHGPH-----DAFRA------- 583
           |      :||| |        ||:||          | |        |     | | |
Db    1093 LLRHAALVLLAGPSDSPLRGGALALL-------VQDPDCRDRHLPAALDLFAACDPYLPP 1145

Qy     584 -SLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFR----TVPVFTLPSQLPDFLGAL 638
            :::  ||         |   : |   ||| |||  || |     | |  |   ::   :|
Db    1146 SAVAAALPTH-----PEPVLEAFRARLLGPDAGEALRRLADATTPALT--HRVAALVGRT 1198

Qy     639 QQPRAPRSGRLQERAEQVSRAL--QPALDSYFHPPGT------PAPGRGVGPGAGPGAGD 690
              _|_ :| |  |  | | |   || :   | |        | | |     ||  | |
Db    1199 VTERPETAGHL---AAYVDRRLDRDPAPRAVLLPLVTRLLDDGPEPARAA--LAGVLAAD 1253

Qy     691 G 691
           |
Db    1254 G 1254


RESULT 7
Q8VII1
ID   Q8VII1      PRELIMINARY;      PRT;  1665 AA.
AC   Q8VII1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   PDZ-domain protein scribble.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=CEREBELLUM;
RA   Mattock K.L., Kurschner C.;
RT   "Molecular cloning of mouse Scribble cDNA.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF441233; AAL32469.1; -.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR003591; LRR_typ.
DR   InterPro; IPR001478; PDZ.
DR   Pfam; PF00560; LRR; 13.
DR   Pfam; PF00595; PDZ; 4.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00369; LRR_TYP; 13.
DR   SMART; SM00228; PDZ; 4.
DR   PROSITE; PS50106; PDZ; 4.
SQ   SEQUENCE   1665 AA;  179749 MW;  BE1272F4ECBF010E CRC64;

  Query Match             3.1%;  Score 116.5;  DB 11;  Length 1665;
  Best Local Similarity   23.5%;  Pred. No. 1.5;
  Matches  140;  Conservative   49;  Mismatches  241;  Indels  167;  Gaps   30;

Qy     126 VLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQ------- 178
           ||     : |:    |||                |: : | | ||     : | :
Db    1172 VLVCDGFDTSTTTALEVS-----------PGVIANPFAAGLGHRNSLESISSIDRELSP 1219

Qy     179 --PRYEKELNHTQQLPALPWLNVSAD--GDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPR 234
             |  ||||       |||| : ||:  | |:                | | :  :   |
Db    1220 EGPGKEKEL----ASQALPWESESAETTGRNLE----------PLKLDYRALAALPSAG 1264

Qy     235 WHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLL 294
           :   ||   |    |   ||         | | :|        |   | | ||
Db    1265 SLQR--GPSATTGGKTTEAPC--------SPGSQQTK-------PGVIQPLAQA------ 1301

Qy     295 TLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENV--TVDKVLEFPLLKGHPNL 352
           |    | : ||       |  || || | |     ||          | :   |
Db    1302 ----W----PRNSPAP-----RGRGG-PCSPPSPDELPANVKQAYRAFAAVPTVHPPENS 1347

Qy     353 CVQ------VNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLP 406
           |        | |:|  :|          :     || | ||       :  |   |
Db    1348 ATQPPTPGPAASPEQLSFRE----------RQKYFELEVRVPQAEGPPKRVSLVGADDLR 1397

Qy     407 SKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKY-IHKRWALVWLACLLFAA 465
                 | :| :   | |:        |  | :    | |:    : ||:
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Db   1398 KMQEEEARKLQQKRAQMLREEAVTSGPDMGLASDRESPDDQQEAEQPWAV---------- 1447

Qy    466 ALSLILLLKKDHAKAAA-------RGRAALLLYSADDSGFERLVGALASALCQLPLRVAV 518
                  ||  ::        | | :    |:    |||   : |     | | |:
Db   1448 ---------PSHAGGSSPSSPPPLGGNAPVRTAKAERRHQERL--RMQSPELPAPER-AL 1495

Qy    519 DLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPH 578
          || | |:    |  | | ::|::  :   :           |     | |  ||
Db   1496 SPAERRALEAEKRALW-RAARMKSLEQDALRAQMV----------LSKSQEGRGKRGPL 1543

Qy    579 DAFRASLS-------CVLPDF-LQ-----GRAPGSYVGACFDRLLHPDAVPALFRTVPVF 625
          :    : |          | || ||     || | |  |  ||      |  ||  : ||:
Db   1544 ERLAEAPSPAPTPSPTPLEDFGLQTSASPGRLPLS--GKKFDY----RAFAALPSSRPVY 1597

Qy    626 TLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGP 682
          :  | |||:  |:   |  |   ||   :|:  |           | |:||  |||
Db   1598 DI--QSPDFVEELRTLEASPSPGSQEEDGEVALVLL----------GRPSPG-AVGP 1641


RESULT 8
Q96M86
ID   Q96M86      PRELIMINARY;      PRT;  1021 AA.
AC   Q96M86;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA FLJ32752 fis, clone TESTI2001661, weakly similar to dynein beta
DE   chain, flagellar outer ARM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RA   Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA   Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA   Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA   Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA   Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA   Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA   Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK057314; BAB71423.1; -.
DR   InterPro; IPR004273; Dynein_heavy.
DR   Pfam; PF03028; Dynein_heavy; 1.
SQ   SEQUENCE   1021 AA;  112942 MW;  A1207BD978EA4D0D CRC64;

  Query Match             3.1%;  Score 116;  DB 4;  Length 1021;
  Best Local Similarity   24.0%;  Pred. No. 0.86;
  Matches  183;  Conservative   75;  Mismatches  276;  Indels  228;  Gaps   44;

Qy     55 PAPGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVE 114
          |||||   |  |  :|:|      :   ||  |:          | ||  :   | :
Db    294 PAPGPGPEPLSLLQKLILWRVLRPE---CLAGALADFTTSLLGRPLDENTY---APTMPF 347

Qy    115 EPRNASLQAQVVLSFQAYPTARC-VLLEVQVPAALVQFGQSVGSVVYDCFEAALGSE--- 170
          :   |:    ::|    :|:|    |  :|  ||  | ||    |:      |||||
Db    348 KHSQATQPMLILLPPPGHPSATLHPLTVIQKLAAKYQQGQKQLQVI------ALGSEAWD 401

Qy    171 ---VRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQV 227
             | : : :|  ||    |        || :    || ||:
Db    402 PVSVVVSTLSQAMYE---GH--------WLVL----DNCHLM----------------- 428

Qy    228 QGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLW- 286
          | | | |    :  |    :|  |  :    :|:|   |:     | |    ||
Db    429 -----PHWPKELLQLLLELLGRAKVVADLESEQLLDQPES--RNVSTVHRDFR----LWL 477

Qy    287 ------QAARLRLLTLQS----W---------LLDAPCSLPAEAALCWRAPGGDPCQPLV 327
                |:   :||  |    |         |:|   |:     : :  |   | | |
Db    478 IVPAESSASLPAVLTQHSMPVFWNQSLELGHVLID---SVELAQQVLYMQP---PTQAL- 530

Qy    328 PPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSL-------------- 373
          | |    : : : |    |: |     ||  :: || |: ||| ||
Db    531 PLLLLHGLLLHRQLYGTRLQAHRGRWSQVTLTQVLQTQDQLWA-SLSNPRAAMQELAASV 589

Qy    374 ---GPLKD----DVLLLETRG-----------PQDNRSLCA-LEP----------SGCTS 404
             ||| |    : |: |:              |   :|| | | |          : | :
Db    590 FYGGPLGDTEDREALISLTQACLSPSSGSWVQPHTPQSLLATLMPLPELRELDAMAECKA 649

Qy    405 ----LPSKASTRAARLGE-----------YLLQDLQSGQCLQLWDDDLGALWACPMDKY 448
              |||    |   | |             || ||    : : :   ||  |   ::
Db    650 QMHLLPSPPEPRLCGLSEGPQAWLLRRQSRALLSALQRSSPVWVPESRRGAQLA---ERR 706

Qy    449 IHKRWALVWLACLLFAAALSLILLLKKDHAKA--------AARGRAALLLYSADDSGFER 500
          : :|  || :   | :    |  ::::| : |        | |    :|   | :    :
Db    707 LRQR--LVQVNRRLESLQDLLTHVIRQDESDAPWSVLGPNARRPLEGVLETEALE--LSQ 762

Qy    501 LVGALASAL-CQL---------PLR----VAVDLWSRR---------ELSAQGPVAWFHA 537
          ||| |   | | |         | |    ||  ||: |           | |  |
Db    763 LVGTLQRDLDCLLQQLKGAPPCPSRRCAAVAHALWTGRLPLPWRPHAPAGPQPPWHWL-- 820

Qy    538 QRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSGPGAHGPH-DAFRASLSCVLPDFLQGR 596
            ||  : | ::|     ||          |  |       |  |||     :|   |:|
Db    821 --RQLSRRGQLLVRYLGVGA---------DASSDVPERVFHLSAFRHPRRLLLA--LRGE 867

Qy    597 A-----------PGSYVGACFDRL----LHPDAVPALFRTV--PVFTLPSQ--LPDFLGA 637
          |           |||  |:   :|    |  :: |  ||    |  |:| :  |   |
Db    868 AALDQNVPSSNFPGSR-GSVSSQLQYKRLEMNSNPLHFRVENGPNPTVPERGLLLIGLQV 926

Qy    638 LQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGT---PAP 676
          |     | :| ||:        | |   |    |||   |||
Db    927 LHAEWDPIAGALQDSPSSQPSPLPPVSIS-TQAPGTSDLPAP 967


RESULT 9
Q8XED7
ID   Q8XED7      PRELIMINARY;      PRT;  745 AA.
AC   Q8XED7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   YehQ protein.
GN   YEHQ OR Z3295 OR ECS2931.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; AE005439; AAG57188.1; -.
DR   EMBL; AP002560; BAB36354.1; -.
KW   Complete proteome.
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FT   CONFLICT    704    704       H -> Y (IN REF. 2).
SQ   SEQUENCE   745 AA;  82593 MW;  37F8C754DE811F43 CRC64;

  Query Match             3.1%;  Score 115.5;  DB 16;  Length 745;
  Best Local Similarity   21.4%;  Pred. No. 0.63;
  Matches  162;  Conservative   70;  Mismatches  234;  Indels  291;  Gaps   43;

Qy      21 LERLVGPQDATH------CSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELVLRC 74
Db     110 LEELATLPDATRKRAQVLVAKGITIELF-----CAPGEIPSARLP-MSDVRFYSRSSIRF 163

Qy      75 QKETDC---DLCLRVAVHLAVHGHWEEPEDEEKF-----------GGAADSGVEEPRNA 119
Db     164 AR-CDCIEGTLCEHVV--LAVQAFVEAKTQQAEFTHLIWQMRSEHVTSSDDPFASEEGNA 220

Qy     120 SLQ--------------AQVVLSFQA------YPTARCVLLEVQVPAALVQFGQSVGSVV 159
Db     221 CRQYVQQLSQALWLGGISQPLIHYEAAFSRAQQAAERCNWR--WVSESLRQLRASV---- 274

Qy     160 YDCFEAA-----LGSEVRIWSYTQPRYEKELNHTQQL---------PALPWLNVSADG-- 203
Db     275 -DAFHARASHYHAGECLRQLAALNSR----LNCAQEMARRDSVGEVPPVPWRTVVGSGIA 329

Qy     204 -----DNVHLV-LNV---SEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVP 254
Db     330 GEAKLDHLRLVSLGMRCWQDIEHYGLRIWF--------------TDPDTGSILHLS--- 371

Qy     255 CLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWLL--------DAPCS 306
Db     372 --------------------RSWPRSEQENSPAATRRLFSFQAGALAGGQIVSQAAKRS 410

Qy     307 LPAEAALCWRAPGGDPCQPLVP--PLSWENVTVDKVLEFPL-----------LKGHPNLC 353
Db     411 ADGELLLATR----NRLSSVVPLSPDAW------RMLSAPLRQPGIVALREYLRQRPPSC 460

Qy     354 V----QVNSSEKLQLQECL---WADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLP 406
Db     461 IRPLNQVDNLFILPVAECISLGWDSSRQTL--DAQVISGEG-EDN--LLTL------SLP 509

Qy     407 SKASTRAA--RLGEYLLQDLQSGQCL----------------------QLWDDD----- 436
Db     510 ASASAPYAVERMAA-LLQQTDDPVCLVSGFVSFVDGQLTLEPQVMMTKTRAWALDAETAP 568

Qy     437 ----LGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKD--HAKAAARGRAALLL 490
Db     569 VVASLPSASVLPVPSTAHQ---------LLMRCQALLIQLLHNGWRYQEQSAIGQAELLA 619

Qy     491 YSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVV 550
Db     620 NDLTAVGFYRLAHVL-----------------------------GQFRNTESEARVEA 648

Qy     551 LLFSPGAVALCSEWL----QDGVSGPGAHG---------PHDAFR---ASLSCVLPDFLQ 594
Db     649 M---NNGVLLCEQLFPLLQQQGLNRPGFPGECFICELRLPDHRFRWKHNKLFLLLPE--- 702

Qy     595 GRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQL 631
Db     703 --------------EHGPAFPAI---VDCYTSPPTL 721


RESULT 10
Q9EYF6
ID   Q9EYF6       PRELIMINARY;      PRT;   745 AA.
AC   Q9EYF6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 82.6 kDa protein.
GN   YEHQ.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7;
RX   MEDLINE=20564182; PubMed=11111050;
RA   Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
RA   Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,
RA   Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,
RA   Shinagawa H.;
RT   "Complete nucleotide sequence of the defective Sakai-VT1 prophage
RT   carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia
RT   coli O157:H7 derived from the Sakai outbreak.";
RL   Gene 258:127-139(2000).
DR   EMBL; AP000400; BAB19549.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   745 AA;  82619 MW;  37EC82409B811F43 CRC64;

  Query Match             3.1%;  Score 114.5;  DB 2;  Length 745;
  Best Local Similarity   21.6%;  Pred. No. 0.76;
  Matches  163;  Conservative   69;  Mismatches  236;  Indels  287;  Gaps   43;

Qy      21 LERLVGPQDATH------CSPGLSCRLWDSDILCLPGDIVPAPGPVLAPTHLQTELVLRC 74
Db     110 LEELATLPDATRKRAQVLVAKGITIELF-----CAPGEIPSARLP-MSDVRFYSRSSIRF 163

Qy      75 QKETDC---DLCLRVAVHLAVHGHWEEPEDEEKF-----------GGAADSGVEEPRNA 119
Db     164 AR-CDCIEGTLCEHVV--LAVQAFVEAKTQQAEFTHLIWQMRSEHVTSSDDPFASEEGNA 220

Qy     120 SLQ--------------AQVVLSFQA------YPTARCVLLEVQVPAALVQFGQSVGSVV 159
Db     221 CRQYVQQLSQALWLGGISQPLIHYEAAFSRAQQAAERCNWR--WVSESLRQLRASV---- 274

Qy     160 YDCFEAA-----LGSEVRIWSYTQPRYEKELNHTQQL---------PALPWLNVSADG-- 203
Db     275 -DAFHARASHYHAGECLRQLAALNSR----LNCAQEMARRDSVGEVPPVPWRTVVGSGIA 329

Qy     204 -----DNVHLV-LNV---SEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVP 254
Db     330 GEAKLDHLRLVSLGMRCWQDIEHYGLRIWF--------------TDPDTGSILHLS--- 371

Qy     255 CLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWLL--------DAPCS 306
Db     372 --------------------RSWPRSEQENSPAATRRLFSFQAGALAGGQIVSQAAKRS 410

Qy     307 LPAEAALCWRAPGGDPCQPLVP--PLSWENVTVDKVLEFPL-----------LKGHPNLC 353
Db     411 ADGELLLATR----NRLSSVVPLSPDAW------RMLSAPLRQPGIVALREYLRQRPPSC 460

Qy     354 V----QVNSSEKLQLQECL---WADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLP 406
Db     461 IRPLNQVDNLFILPVAECISLGWDSSRQTL--DAQVISGEG-EDN--LLTL------SLP 509

Qy     407 SKASTRAA--RLGEYLLQDLQSGQCL----------------------QLWDDD----- 436
Db     510 ASASAPYAVERMAA-LLQQTDDPVCLVSGFVSFVDGQLTLEPQVMMTKTRAWALDAETAP 568

Qy     437 ----LGALWACPMDKYIHKRWALVWLACLLFAAALSLILLLKKD--HAKAAARGRAALLL 490
Db     569 VVASLPSASVLPVPSTAHQ---------LLMRCQALLIQLLHNGWRYQEQSAIGQAELLA 619

Qy     491 YSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVV 550
Db     620 NDLTAVGFYRLAHVL-----------------------------GQFRNTESEARVEA 648

Qy     551 LLFSPGAVALCSEWL----QDGVSGPGAHGPHDAFRASLSCVLPD----------FLQGR 596
Db     649 M---NNGVLLCEQLFPLLQQQGLNRPGF--PGECFICELR--LPDHRFRWKHNKLFL--- 698

Qy     597 APGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQL 631
Db     699 ------------LLPEEYGPAFPAIVDCYTSPPTL 721
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RESULT 11
Q9HZE5
ID   Q9HZE5      PRELIMINARY;      PRT;  1193 AA.
AC   Q9HZE5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Hypothetical protein PA3063.
GN   PA3063.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004730; AAG06451.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   1193 AA;  135097 MW;  1FE9553F34D3C191 CRC64;

  Query Match             3.1%;  Score 114.5;  DB 16;  Length 1193;
  Best Local Similarity   21.7%;  Pred. No. 1.4;
  Matches  154;  Conservative   53;  Mismatches  240;  Indels  263;  Gaps   38;

Qy      81 DLCLRVAVHLAVHGHWE--------EPEDEEKFGGAADSGV---EEPRNASLQAQVV--- 126
           || | :|    |   ||         |||       |  |      ||      |::
Db     293 DLRLNMAAG-RVERAWEVGQELLALRPEDRTLLADLARLGEWTGNGPRALGFWKQLLAGA 351

Qy     127 -----------LSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIW- 174
                      || | :    : |   : |     : : ::||       |   |
Db     352 DDPALREHAWRLSLQMFDFDSAIELLAPIGAQRQMTDEELDALVYSHETRGTPEEGEAWL 411

Qy     175 -SYTQPRYEKE----------LNHTQQLPALP--WLNVSADGDNVHLVLNVSEEQHFGLS 221
            | | || |:          | |||||      |  ::      |  |:| |   :
Db     412 RGYVQ-RYPKQRLAWQRLQQILEHTQQLQEETGVWARMAR-----HFPLSVKERMQWA-E 464

Qy     222 LYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPD------------SV 268
           :||     |:  | | | |     :   :         | || |             :
Db     465 THWNLFD--PRQAW-KVLAGVDTRAIREPEFWRLRAALAWALEQDDDARAAYERMLALDI 521

Qy     269 RTN-------ICPFRED--PRAHQNL---WQAAR-----LRLLTLQSWLLDAPC--SLPA 309
           | |       |  :|:    :| | |   || :|       | |   | | |   || |
Db     522 RLNSRDEDQLIALYRDSNPKQALQVLIGSWQRSRDPRRLASALQLAENLHDWPALKSLLA 581

Qy     310 EAALCWRAPGGDPCQPLVPPLSW----------------ENVTVDKVLEFPLLKGHPNLC 353
           ||     | |         |  |                | :  : :: ||
Db     582 EAEGLPEAQGS--------PYYWVARARLAEQEGHGDVAERLYREALVRFP--------- 624

Qy     354 VQVNSSEKLQLQECLW-------ADSLGP---------LKDDV---------LLLETRGP 388
                 | |  :  ||        |||  |         |:|            ||||
Db     625 -----GENLVRERLLWFYIDRGRRDSLAPLLAQWHGLALRDSTLWLPFASASLLLE---- 675

Qy     389 QDNRSLC--------------------ALEPSGCTSLPSKASTRAARLGEYLLQDLQSG 427
           :::::|                    ||: ||          :| ||   ||: |
Db     676 RNDQALAWFRLYLKSNPNDWLVQAAYADALDASG-------YQDKALRLRRLLLRRL--- 725

Qy     428 QCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLIL-----LLKKDHAKAAA 482
                 |  |: | |                  ||  | |:          || :  |: |
Db     726 --------DREAVRATPDS---------------FATYLRLLAVAQGPLLAQGEARRAW 761

Qy     483 RGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQT 542
           |  |:|         ||: :  || |  | ||:   | |           :||   :  :
Db     762 NGEPAML-----QLWFEQFLDQLA-ATNQEPLK---DNW----------LAWARGRGLKI 802

Qy     543 LQEGGVVVLLFSPGAVALCSEWLQDGVSGPG---------AHGPHDAFRASLSCVLPDFL 593
           :   :   | |    ||    |: |   |            ||
Db     803 GRNEEIQAALRSQNRAAL-QRLLERGELDPAQRVEALVRLGHG---------------- 844

Qy     594 QGRAPGSYVGACFD-------RLLHPDAVPALFRTVPVFTLPSQLPDFLG 636
           | | |  :||  |          |   |   | ||     |    || |
Db     845 -GEALGEALGALGDGHSRDNREQLRRQAAEILERTPQGLQLGWNKRDFGG 893


RESULT 12
Q96DW2
ID   Q96DW2      PRELIMINARY;      PRT;   657 AA.
AC   Q96DW2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RecQ protein-like 4 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LYMPH;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013277; AAH13277.1; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR001650; Helicase_C.
DR   Pfam; PF00271; helicase_C; 1.
KW   ATP-binding; Helicase.
FT   NON_TER       1       1
SQ   SEQUENCE   657 AA;  73415 MW;  CF51B910F560CA18 CRC64;

  Query Match             3.0%;  Score 112.5;  DB 4;  Length 657;
  Best Local Similarity   19.6%;  Pred. No. 0.95;
  Matches  115;  Conservative   73;  Mismatches  194;  Indels  205;  Gaps   31;

Qy      16 PVVLSLERLVGPQDATHCSPGLSC---RLWDSDIL--CLPGDIVPAPGPVLAPTHLQ--- 67
           |  | : :::  :   ||  ||:    |   ||:       :     ||   ||:|
Db      68 PCYLRVCKVLRERMGVHCFLGLTATATRRTASDVAQHLAVAEEPDLHGPAPVPTNLHLSV 127

Qy      68 ----------------------TELVLRCQKETDCDLCLRVAVHL--AVHGHWEEPEDEE 103
                                  ::: | :  | :   |:|  |   :|  |
Db     128 SMDRDTDQALLTLLQGKRFQNLDSIIIYCNRREDTE---RIAALLRTCLHAAWVPGS--- 181

Qy     104 KFGGAADSGVEEPRNASL--------------QAQVVLSFQAY------PTARCVLLEV 142
             || |     |  :| :                | :||::  |:      |  | | | :
Db     182 --GGRAPKTTAEAYHAGMCSRERRRVQRAFMQGQLRVVVATVAFGMGLDRPDVRAV-LHL 238

Qy     143 QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYE--KELNHTQQLPALPWLNVS 200
           :| :   : |:||     |       |       : ||: |  :||       :  :| |
Db     239 GLPPSFESYVQAVGRAGRD------GQPAHCHLFLQPQGEDLRELRRHVHADSTDFLAVK 292

Qy     201 ADGDNVHLVLNV------------SEEQHFGLSLYWNQVQGP-PKPRW---------HKN 238
                 ||  |             ||::          | |  | |::         |:
Db     293 ------RLVQRVFPACTCTCTRPPSEQE--------GAVGGERPVPKYPPQEAEQLSHQA 338

Qy     239 LTGPQIITLNHTDLVPC-LCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLL--T 295
           ||: : : |   :|  | :|   :  ::: | :|         | : |    | ||  |
Db     339 APGPRRVCMGHERALPIQLTVQALDMPEEAIETLLCYL----ELHPHHW----LELLATT 390

Qy     296 LQSWLLDAPCSLPAEAALCWRAP----------GGDPCQ----------PLVPPLSWENV 335
                |: |        ||  | |             || |             ||  : ||
Db     391 YTHCRLNCPGGPAQLQALAHRCPPLAVCLAQQLPEDPGQGSSSVEFDMVKLVDSMGWELA 450

Qy     336 TVDKVL--------------------EFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
           :| : |                    ||  |  |       : : || |: : |:    |
Db     451 SVRRALCQLQWDHEPRTGVRRGTGVLVEFSELAFHLRSPGDLTAEEKDQICDFLY----G 506

Qy     375 PLKDDVLLLETRGPQDNRSLCALE----------PSGCTSLPSKASTRAAR----LGEY 419
           ::          :: ::|  |            ||    |  :   |: |    || |
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Db    507 RVQ----------ARERQALARLRRTFQAFHSVAFPSCGPCLEQQDEERSTRLKDLLGRY 556

Qy    420 L----------LQDLQS---GQC-LQLWDDDLGALWACPMDKYIHKR 452
                      ::| |    ||  || |:| :     | : :::  |
Db    557 FEEEEGQEPGGMEDAQGPEPGQARLQDWEDQV----RCDIRQFLSLR 599


RESULT 13
Q96F55
ID   Q96F55      PRELIMINARY;      PRT;   744 AA.
AC   Q96F55;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RecQ protein-like 4 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011602; AAH11602.1; -.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR001650; Helicase_C.
DR   InterPro; IPR004589; RecQ.
DR   Pfam; PF00270; DEAD; 1.
DR   Pfam; PF00271; helicase_C; 1.
DR   TIGRFAMs; TIGR00614; recq; 1.
KW   ATP-binding; Helicase.
FT   NON_TER       1       1
SQ   SEQUENCE   744 AA;  82839 MW;  6AE0F90340A2C9F1 CRC64;

  Query Match             3.0%;  Score 112.5;  DB 4;  Length 744;
  Best Local Similarity   19.6%;  Pred. No. 1.1;
  Matches  115;  Conservative   73;  Mismatches  194;  Indels  205;  Gaps   31;

Qy     16 PVVLSLERLVGPQDATHCSPGLSC---RLWDSDIL--CLPGDIVPAPGPVLAPTHLQ--- 67
          |  | : :::  :   ||  ||:    |   ||:       :     ||   ||:|
Db    155 PCYLRVCKVLRERMGVHCFLGLTATATRRTASDVAQHLAVAEEPDLHGPAPVPTNLHLSV 214

Qy     68 ----------------------TELVLRCQKETDCDLCLRVAVHL--AVHGHWEEPEDEE 103
                                :::| :  | :   |:|  |   :|  |
Db    215 SMDRDTDQALLTLLQGKRFQNLDSIIIYCNRREDTE---RIAALLRTCLHAAWVPGS--- 268

Qy    104 KFGGAADSGVEEPRNASL--------------QAQVVLSFQAY------PTARCVLLEV 142
            || |     |  :| :                | :||::  |:       |  | | | :
Db    269 --GGRAPKTTAEAYHAGMCSRERRRVQRAFMQGQLRVVVATVAFGMGLDRPDVRAV-LHL 325

Qy    143 QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYE--KELNHTQQLPALPWLNVS 200
           :| :   : |:||    |       |       : ||: |  :||         :  :| | |
Db    326 GLPPSFESYVQAVGRAGRD------GQPAHCHLFLQPQGEDLRELRRHVHADSTDFLAVK 379

Qy    201 ADGDNVHLVLNV------------SEEQHFGLSLYWNQVQGP-PKPRW---------HKN 238
              ||  |             ||::         | |  | |::          |:
Db    380 ------RLVQRVFPACTCTCTRPPSEQE--------GAVGGERPVPKYPPQEAEQLSHQA 425

Qy    239 LTGPQIITLNHTDLVPC-LCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLL--T 295
            ||: : : |   :|  | :|   :  ::: | :|        | : |    | ||  |
Db    426 APGPRRVCMGHERALPIQLTVQALDMPEEAIETLLCYL----ELHPHHW----LELLATT 477

Qy    296 LQSWLLDAPCSLPAEAALCWRAP----------GGDPCQ----------PLVPPLSWENV 335
            |: |       ||  | |              || |           ||  : ||
Db    478 YTHCRLNCPGGPAQLQALAHRCPPLAVCLAQQLPEDPGQGSSSVEFDMVKLVDSMGWELA 537

Qy    336 TVDKVL--------------------EFPLLKGHPNLCVQVNSSEKLQLQECLWADSLG 374
          :| : |                    ||  |  |      : : || |: : |:    |
Db    538 SVRRALCQLQWDHEPRTGVRRGTGVLVEFSELAFHLRSPGDLTAEEKDQICDFLY----G 593

Qy    375 PLKDDVLLLETRGPQDNRSLCALE----------PSGCTSLPSKASTRAAR----LGEY 419
          ::          :: ::|  |            ||    |  :   |: |    || |


Db    594 RVQ----------ARERQALARLRRTFQAFHSVAFPSCGPCLEQQDEERSTRLKDLLGRY 643

Qy    420 L----------LQDLQS---GQC-LQLWDDDLGALWACPMDKYIHKR 452
                      ::| |    ||  || |:| :     | : :::  |
Db    644 FEEEEGQEPGGMEDAQGPEPGQARLQDWEDQV----RCDIRQFLSLR 686


RESULT 14
Q8TZU1
ID   Q8TZU1      PRELIMINARY;      PRT;   405 AA.
AC   Q8TZU1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein PF1892.
GN   PF1892.
OS   Pyrococcus furiosus.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Pyrococcus.
OX   NCBI_TaxID=2261;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA   Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT   "The complete sequence of the Pyrococcus furiosus genome.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE010284; AAL82016.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   405 AA;  46019 MW;  C68F3700FF1C615F CRC64;

  Query Match             3.0%;  Score 111.5;  DB 17;  Length 405;
  Best Local Similarity   22.0%;  Pred. No. 0.61;
  Matches   87;  Conservative   51;  Mismatches  130;  Indels  127;  Gaps   21;

Qy    325 PLVP-----------PLSWENVTVDKVLEFP--LLKGHPNLCVQVNSSEKL--QLQECLW 369
          ||||           ||||||| :: |: |    |: |   : | |  | ||   |||
Db     64 PLVPPIQGDTQYMDSPLSWENVRIEDVIRFRSLLVLGEAKVNVDVRKSSKLIDSLQEL-- 121

Qy    370 ADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQC 429
          | |: |:  :|:| |                :|:    || : :      |:        :
Db    122 AMSIKPVDSEVILKE-------------KPA-INILPEEFAPPLGPRGKL--------KV 159

Qy    430 LQLWDDDLGALWACP--MDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRAA 487
           :: |:        |  :|| |                              |  ||    | |
Db    160 FKVVDNP-----KVPRKVDKTI------------------------SDELKA----REA 185

Qy    488 LL-LYSADDSGFER--LVGALASALCQLPLRVAVDLWS------------RRELSAQGPV 532
          :: ||   :|||:   ::  |:: |  :  |:    ||             |: :     :
Db    186 IIGLY---ESGFDEYYIIRLLSAGLLGVKKRIVPTRWSITAVQDTIGNYLRKNILKNPII 242

Qy    533 AWFHAQRRQTLQEGGVVVLLFSPGAVALCSEWLQD---GVSGPGAHGPHDAFRASLSCVL 589
            |     : |.   ||:||    :  |   ||:    | | |      :: ||
Db    243 DNFEVYHHEFLGNRYVVLLLPMTYSFELLEVWLKGSLFGTSKPSVIHDYEDFRG------ 296

Qy    590 PDFLQGRA---PGSYVGACFDRL------------LHPDAVPALFRTVPVFTLPSQLPD 633
             |:| |    |:|  |    |              :  :  || :  | |: :   :
Db    297 ---LKGYAEQTTGAYYAARLSVLEYLRKRKRQAGIIVFREVTPAYYAPVGVWQIRVGVKK 353

Qy    634 FLGALQQPRAP-RSGRLQERAEQVSRALQPALDSY 667
          |      : | :   | |   |:   |:  | |
Db    354 AL-----EKGPIKFENLAEALNQIGNILEHPLEEY 383


RESULT 15
Q9RY89
ID   Q9RY89      PRELIMINARY;      PRT;   478 AA.
AC   Q9RY89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein DR0061.
GN   DR0061.
OS   Deinococcus radiodurans.
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OC   Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC   Deinococcaceae; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1;
RX   MEDLINE=20036896; PubMed=10567266;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
DR   EMBL; AE001869; AAF09658.1; -.
DR   TIGR; DR0061; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   478 AA;  51231 MW;  5E74CDEB8FBA5C95 CRC64;

  Query Match             3.0%;  Score 111.5;  DB 16;  Length 478;
  Best Local Similarity   25.7%;  Pred. No. 0.76;
  Matches  105;  Conservative   39;  Mismatches  145;  Indels  119;  Gaps   20;

Qy     276 REDPRAHQNLWQAARLRLLTLQSWLL--------DAPCSLPAEAALCWRAPGGDPCQPLV 327
Db     110 RADPRERPLLREAAQ----RIRRWLARRLARAPGQLPGTVPAHSVLY----AQEEASALS 161

Qy     328 PPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKDDVLLLETRG 387
Db     162 APAAGDGLT--------LHLGGPD---RLAHWQGLRLS---WR-SLGPNWQLLVQDETSQ 206

Qy     388 PQDNRSLCALEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDK 447
Db     207 PVSGGQLALLRP----DLPASERQLFLTVGGQQLQVLFSG-----------------DY 244

Qy     448 YIHKRWALVWLACLLFAAALSLILLLKKDHAKAAARGRA-ALLLYSADDSGFERLVGALA 506
Db     245 VLLRRRA---------DAAQTRHL------ARLAALGRACALLLLPAEQHGRLRLARTLA 289

Qy     507 SALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRQTLQEGGVVVLLFSPGAV-------- 558
Db     290 RRLRGDPPR-ADDPASGQVAFAQTPAECLAAARR-SLQRLEPLLGRFSPAQVAHEAQVAQ 347

Qy     559 --------------------ALCSEWLQDGVSGP--GAHGPHDAFRASLSCVL----PDF 592
Db     348 ALLHLPPHYAAQVQQAAEHAASAAEPLREAATDPLVGREAGPPVLPATGHFIVFPLGPDP 407

Qy     593 LQGRAPGSYVGACFDRL--LHPDAVPALFRTVPVFTLPSQLPDFLGAL 638
Db     408 LEVRLPG-------DRLLTLRPD-----YRAELVAVLPGQAAVTVGDL 443


Search completed: February 24, 2003, 09:24:47
Job time : 52 secs
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